

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 13.5644 Seconds
(without alignments)
1545.568 Million cell updates/sec

Title: US-09-911-777-1

Perfect score: 1116

Sequence: 1 MDDSTERQSRITSLCKRE.....ENAIQLDGDVTFFGALKLL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	8.2	1121	2 S57058	probable membrane
2	88	7.9	664	1 WMBEBH	infected cell prot
3	87.5	7.8	240	1 S76714	hypothetical prote
4	85	7.6	213	2 C81874	hypothetical prote
5	84.5	7.6	637	2 S36523	E1 protein - human
6	84	7.5	563	2 F95076	sensor histidine k
7	84	7.5	563	2 C97944	histidine kinase (
8	83.5	7.5	360	2 G64575	conserved hypothet
9	83.5	7.5	596	2 B96834	hypothetical prote
10	83.5	7.5	630	1 W1WL35	E1 protein - human
11	83	7.4	218	2 D81148	conserved hypothet
12	82.5	7.4	228	2 T01350	hypothetical prote
13	82.5	7.4	737	1 K1PTCE	protein kinase C (
14	82	7.3	620	2 JH0821	95K golgi antigen
15	81.5	7.3	737	1 K1M521	protein kinase C (
16	81.5	7.3	760	2 S55520	chitin synthase (E
17	80.5	7.2	325	2 S35303	superantigen Mtv -
18	80.5	7.2	577	2 B4307	phosphoprotein pho
19	79.5	7.1	330	2 F75410	conserved hypothet
20	79	7.1	533	2 F75583	GGDEF family prote
21	78.5	7.0	330	2 T47576	FKBP12 interacting
22	78	7.0	233	2 S11688	tumor necrosis fac
23	78	7.0	233	2 T02390	citrate (ci)-synth
24	78	7.0	1655	2 T13998	gene mastermind pr
25	77.5	6.9	320	2 S26387	superantigen Mtv9
26	77.5	6.9	320	2 AF3237	transcriptional re
27	77.5	6.9	356	2 B30338	late competence pr
28	77.5	6.9	889	2 B55123	coatamer complex b
29	77	6.9	431	2 S56228	alpha-factor recep

30 77 6.9 665 2 B82506
31 76.5 6.9 737 1 S28942
32 76.5 6.9 877 1 A25962
33 76.5 6.9 1208 2 A31947
34 76 6.8 378 1 OKGARI
35 76 6.8 473 2 D83246
36 76 6.8 592 2 C70302
37 76 6.8 674 2 T19268
38 76 6.8 1675 2 T31473
39 75.5 6.8 510 2 D69946
40 75.5 6.8 531 2 T30167
41 75.5 6.8 561 2 S71597
42 75.5 6.8 899 2 S76449
43 75.5 6.8 1490 2 T16086
44 75 6.7 278 2 T46458
45 75 6.7 672 2 H86169

ALIGNMENTS

RESULT 1

S57058

probable membrane protein YJR039w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein J1614

C:Species: Saccharomyces cerevisiae

C>Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002

C:Accession: S57058; S63780

R:Huang, M.E.; Chuat, J.C.; Galibert, F.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S57052

A:Accession: S57058

A:Molecule type: DNA

A:Residues: 1-1121 <MAN>

A:Cross-references: EMBL:Z49538; NID:gl015687; PID:gl015689; MIPS:YJR039w

R:Huang, M.E.; Chuat, J.C.; Galibert, F.

Yeast 11, 775-781, 1995

A:Title: Analysis of a 42.5 kb DNA sequence of chromosome X reveals three tRNA genes and

A:Reference number: S63757; MUID:95397595; PMID:7668047

A:Accession: S63780

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1121 <HUA>

A:Cross-references: EMBL:L36344

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996

A:Cross-references: SGD:S0003800

A:Map position: 10R

A:Note: YJR039w

C:Superfamily: Saccharomyces cerevisiae probable membrane protein YJR039w

C:Keywords: transmembrane protein

Query Match 8.2%; Score 91; DB 2; Length 1121;
Best Local Similarity 25.3%; Pred. No. 4;
Matches 39; Conservative 22; Mismatches 51; Indels 42; Gaps 8;

QY 15 CLKREENKLECVSILPRKSPSVLLSCCLTVSVFYQVAALQGLASRLAELOSHH--A 72

DB 155 CLEE--TDVKLSYVTS-----SPIVSDACINFNDF-----LDKDVFTLSILTRAHNEVA 202

QY 73 EKLPAKAGIFPPAPGEGNSQNSRNRKAVQGPETVTQDCLQLIADSETPTIQKGSYTF 132

DB 203 YKLEACVCFB--SRPAKTKWQRTNLTFFV--EATVSQVLLKSVTNL-----GHFVF 252

QY 133 VFWLLSFKRGSLYQVLYTDKTYAMGHLIQRKK 166

DB 253 TPW-----KTFYFKHALSSKQ 268

RESULT 2

WMBEBH

infected cell protein ICP18.5 - bovine herpesvirus 2 (strain BMV)

C:Species: bovine herpesvirus 2
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Nov-1996
C:Accession: B29242
R:Hammerschmidt, W.; Contraths, F.; Mankertz, J.; Pauli, G.; Ludwig, H.; Buhk, H.J.
Virology 165, 388-405, 1988
A:Title: Conservation of a gene cluster including glycoprotein B in bovine herpesvirus 2
A:Reference number: A94381; MUID:88306231; PMID:2841793
A:Accession: B29242
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-664 <HAM>
A:Cross-references: GB:M21628
C:Superfamily: herpesvirus infected cell protein ICp18.5
C:Keywords: capsid assembly

Query Match 7.9%; Score 88; DB 1; Length 664;
Best Local Similarity 23.5%; Pred. No. 4.1;
Matches 46; Conservative 33; Mismatches 49; Indels 68; Gaps 11;

QY 29 SILPRKESPSVLLSCC---LTVVSFVQVAALQ-GDLASLRAELQGHAEKLPAGAKIFEP 84
DB 394 SAAPDDQTEALVACVNHLSAPVRLQAGSEHGDAELRSALGLHAEADP----- 445
QY 85 PAPGCGNSQSNRKRRAV-QGPEETVTQDCLQIADSETPTIQKGSYTFVFWLLSFKRGS 143
DB 446 --PGDGAKEARRAPSLGGPED-----DWAALAAARAA 477
QY 144 ALYG--QVLYDTKTAMGHILQKVVHFGDELSLVTIFRCIQNLGEGDELQALPRENA 201
DB 478 ADVGARRRLYADR-----LTKR-----SLASLGRVCR--EORGELEKML----- 514
QY 202 QISLDGCV--TFEGAL 215
DB 515 RVSTYGEVLPVFAAV 530

RESULT 3
S76714
hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S76714
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76714
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-240 <KAN>
A:Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PID:g1208490
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Start codon: GTG
C:Superfamily: conserved hypothetical protein MTH1849

Query Match 7.8%; Score 87.5; DB 1; Length 240;
Best Local Similarity 22.8%; Pred. No. 1.3;
Matches 52; Conservative 27; Mismatches 74; Indels 75; Gaps 10;

QY 1 MDDSTERQSRLLTSLCKREKNLKECVSLPRKESPSVLLSCCLTVVSFVQVAALQDGL 60
DB 1 MEPOGQERNVGAIRAMK---NMGLEELVNP-----C-----DY 33
QY 61 ASLRAELQGHAEKLPAGAKIFEPAPGEGNSQ---NSRNKRAVQGPETVTQDCLQLI 117
DB 34 RSVEAQTWAVHAKVDVLAQAKVDDDLATAGRQRIATISARERILQSPMETPRQ----- 87
QY 118 ADSETPTIQKGSYTFVFWLLSFKRGSAL-YGQ--VLYTDKTYAMGHILQKVVHFGDEL 174

DB 88 -----ALFWLAPNLKLSALVFGREDSGLTNEELNQAHFRVRIPVHPQYPSL 133
QY 175 SL-----VTLPRCIQ-----NLEEGDELQALPRENAQI 203
DB 134 NLSQAVWCTYELLYQASLAMEITNNQVPGDRLEDGSTMPLA---TNAQL 178

RESULT 4
C81874
hypothetical protein NMA1086 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup C)
C:Species: *Neisseria meningitidis*
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: C81874
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: C81874
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-213 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CA884349.1; PID:g737974
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1086

Query Match 7.6%; Score 85; DB 2; Length 213;
Best Local Similarity 22.9%; Pred. No. 1.9;
Matches 43; Conservative 30; Mismatches 63; Indels 52; Gaps 8;

QY 72 AEKLPAA-GAKIFEPAPGEGNSONS-----RNKRAVQGPET--- 108
DB 23 SEQVARGVAVINHPNPLQGGTNTNKVIQTAALKSLKGLFHCYLPNLRGCGSEGTHTYG 82
QY 109 --VTQDCLQLI-----ADSETPTIQKGSYTFVFWLLSFKRGSALYGOVL-----YTD 153
DB 83 RGETQDCLAVIDYARAQHPAEPALSGFSGGVATFAAQARIPDLLLLIGAAVCHVTG 142
QY 154 K--TYAMGHILQKVVHFGDELSLVTIFRCIQNLGEGDELQALPRENAQISLDGVTTF 211
DB 143 RPEPSAVPNVAKTLMIHGADEV-----VEIGKALKWAEPDLPVITTAGSTHTF 191
QY 212 F-GALKLL 218
DB 192 FHGKLLVL 199

RESULT 5
S36523
E1 protein - human papillomavirus type 35H
C:Species: human papillomavirus type 35H
C:Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
C:Accession: S36523
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36523
A:Molecule type: DNA
A:Residues: 1-637
A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52563.1; PID:g397000
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E1 protein
C:Keywords: early protein; nucleus

Query Match 7.6%; Score 84.5; DB 2; Length 637;
Best Local Similarity 29.6%; Pred. No. 8.2;
Matches 45; Conservative 16; Mismatches 56; Indels 35; Gaps 8;

QY 19 REEMKKECVSLPRKESPSVLLSCCLTVVSFVQVAALQDGLASLRAELQGHAEKLPAG 78
DB 74 QEOTHKEAVQVLRKYVASSPLSGSVLCVNN-----NISPLKAICICENKNTA 121

RESULT 7
C97944 : histidine kinase (EC 2.7.3.-) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: C97944
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
r, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID: 21429245; PMID:11544234
A:Accession: C97944
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-563 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99383.1; PID:gl5458158; GSPDB:GN00174
C:Genetics:
A:Gene: hk09

Query Match	7.5%;	Score 83.5;	DB 2;	Length 360;
Best Local Similarity	24.0%;	Pred. No. 5.1;		
Matches	56;	Conservative	28;	Mismatches 106; Indels 43; Gaps 11;
QY	1	MDDSTREGRSLTSC	LKGR	EMKLCVSTLPRKSPSVLLSCCLTVVSYFVAALGGDL 60
DB	116	LEDESQDADEIEKAL	KDSNFKL	KERAQKLKELDGK----ECFITLMOYGHMPLLGEL 171
QY	61	A-----SURABELQGH	HAELP--	AGAKITEPPAPGEGNSQNSNRKRAVQG--- 104
DB	172	VSDVFYKPHNESPE	SP	PLKGKHLKEKPFKHNRLVLD-NKPLAWIDVRESKEKRNADGSYYR 230
QY	105	-PSETVTQDCLQIA	DSEPTIQ	KSGSVTFVPWLLSFKRGSALYGOVLYTDTKVAMGHLIQ 163
DB	231	ESIIITAEKCLDFM	KDE-PD	FTFGVITP-----FSEQRKLEQAL---KGYAN---LE 277
QY	164	RKKVHVF-GDELS	VLTRF	CIQNLREG-----DELQLAIPRENAQISLDGD 208
DB	278	IGVVDVFOGKEFD	WFLSSV	RTHTGTFGFLKISSCLCVALSROKRALIVAGD 330

RESULT 9
B96834
hypothetical protein PF6_2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: B96834
R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.;
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creevy, T.H.;

ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzwerg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96834
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-596 <STO>
A:Cross-references: GB:AE005173; NID:g6751702; PIDN:AAF7684.1; GSPDB:GN00141
C:Genetics:
A:Gene: F516.2
A:Map position: 1

Query Match 7.5%; Score 83.5; DB 2; Length 596;
Best Local Similarity 19.3%; Pred. No. 9.4;
Matches 47; Conservative 42; Mismatches 97; Indels 57; Gaps 8;

Qy 12 LTSLCKREEMKLCVSIILPK-----EPPSVLLSCLTVVSYVAALQGD LAS 62
Db 4 LSKVLRRTQRLGACSAVFSKDIQLGERSFDSNSIASTKREAVRFRFYEISLSNRALS 63
Qy 63 LRAELQGHAE-KLPAGAKIPFPAPGEGNSQNSKRAVQGPETVTQDCLQIADSE 121
Db 64 SAGATKSDQEDDLEDGFSELGSKSGQGSTSDDEKLSADEEBEELDLIE--TDVS 121
Qy 122 TPTIQGSGTYFPWLLS---FKRGSAlyGVLYTDKTYAMGH-----LIQRKVVH 168
Db 122 RKTVEKQSELFTKTVSAPGLSIGAL-----DKWVEEGNEITRVIKAMQLRRRR 174
Qy 169 VFG-----DELSLVTFRCTONLEEGDELOLAIPRENAQISLQGD 208
Db 175 MYGRALOMSEWLEANKKIEMTERDYASRLDITVKIRGLEKACQKIPK-----SFKGE 229
Qy 209 VTF 211
Db 230 VLY 232

RESULT 10
W1WL35
E1 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
A:Accession: A40824
R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillo
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: A40824
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-630 <MAR>
A:Cross-references: GB:M74117; NID:g333050; PIDN:AAA46968.1; PID:g333053
C:Superfamily: papillomavirus E1 protein
C:Keywords: early protein

Query Match 7.5%; Score 83.5; DB 1; Length 630;
Best Local Similarity 29.6%; Pred. No. 10;
Matches 45; Conservative 15; Mismatches 57; Indels 35; Gaps 8;

Qy 19 REEMKLEKCVSLPRKESPVLLSCLTVVSYVAALQGD LASRAELQGHAEKLPAG 78
Db 73 QEEQTHKEAVQVLEKYASSPSSVSLCVNN-----NISPLKALCIENKNTA 120
Qy 79 AK--IFEPAPGEGNSQNSKRAVQGPETVTQDCLQIADSE-----ETPT-- 124
Db 121 AKRRLFELPDSGCGYGNSEVIEHIIQQVEG-HDTVEQ-CSMGSGDSITSSSDERHDETPTRD 178

ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzwerg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96834
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-596 <STO>
A:Cross-references: GB:AE005173; NID:g6751702; PIDN:AAF7684.1; GSPDB:GN00141
C:Genetics:
A:Gene: F516.2
A:Map position: 1

Qy 125 ---IQGSGTYFPWLLSFKRGSAlyGVLYTD 153
Db 179 IIQILKCSNANAMLAKEKE---LFG-ISFTE 206

RESULT 11
D81148
conserved hypothetical protein NMB0868 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: D81148
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: D81148
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-213 <TET>
A:Cross-references: GB:AE002439; GB:AE002098; NID:g7226100; PIDN:AAF41279.1; PID:g722610
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0868

Query Match 7.4%; Score 83; DB 2; Length 213;
Best Local Similarity 23.4%; Pred. No. 3;
Matches 44; Conservative 29; Mismatches 63; Indels 52; Gaps 9;

Qy 72 AEKLPK-AKATFEPAPGEGNSQNS-----RNKRAVQGPET--- 108
Db 23 SEQPARGVAVINHPNPLQGTNTNKVIQTAAKSLGHFHYLPNLRGVGGSGGTHDYG 82
Qy 109 --VTQDCLQLI-----ADSETPTIQGSGTYFPWLLSFKRGs-----ALYQVLY--YTD 153
Db 83 RGETQDCLAVIDYARAQHPAPEALSGFSFGGVATFAAQARTPDLLLIGAAVCHYTD 142
Qy 154 K--TYAMGHLIQRKKVHVGDELSTLVTFRCTONLEEGDELOLAIPRENAQISLQGDVTF 211
Db 143 RPEPSAVPNVAKTLMIHGADEV-----VEIGKALKWAEPODLPVITTAGSTHF 191
Qy 212 F-GALKLL 218
Db 192 FHGKLIVL 199

RESULT 12
T01350
hypothetical protein F6N15.4 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 14-May-1999
A:Accession: T01350
R:Ryan, E.; Edwards, J.; Pape, K.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of A. thaliana F6N15.
A:Reference number: Z14297
A:Accession: T01350
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-228 <RYA>
A:Cross-references: EMBL:AF069299; NID:g3193311; PID:g3193318
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 103/3
A:Note: F6N15.4

Query Match 7.4%; Score 82.5; DB 2; Length 228;
Best Local Similarity 25.1%; Pred. No. 3.6;
Matches 46; Conservative 23; Mismatches 63; Indels 51; Gaps 9;

F:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
F:703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

```
Query Match      7.3%; Score 81.5; DB 1; Length 737;
Best Local Similarity 20.7%; Pred: No. 19;
Matches 50; Conservative 33; Mismatches 89; Indels 69; Gaps 10;

QY 19 REEMKKECVSILPRKSPSVLLSCCLTVVSVFYQVAALQGDLSLRAEL--QGHHAELKP 76
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 268 ROGLOCKVKKNVHRCETNPNC---GVDARGIAKVLADLGVTDPDKITNSGQRRKLA 324
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 77 AGAKIFPPAPGEGNS-SONGRNKRKAVOGP-----EETVQDC 113
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 325 AGA---ESPQASGNSPSEDDRSKAPTSPCDQELKELENNIRKALSFDNRGEHRASSA 381
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 114 L--QLIADSETPTIQG-----SYTFVPWLLSFKEGSALYGVLYTDKTYAMGHLIQ 163
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 382 TDGQLASPGENGVEVRPGQAKRLGLDFNFIKVLGKSGFKVMLAELKKGDEVYAV--KVL 439
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 164 RKKVHVFGEELS-----LVTLFRCIQNLE-----EGDELQLAIP 197
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 440 KKDVLQDDDDVDCMTXKRLILARKHPYLTQLYCCFQTKDRLPFVMEYVNGGDLMFQIQ 499
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 198 R 198
   |
Db 500 R 500
```

Search completed: February 3, 2004, 07:45:36
Job time : 16.5644 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 9.20444 Seconds
(without alignments)
1113.790 Million cell updates/sec

Title: US-09-911-777-1

Perfect score: 1116

Sequence: 1 MDDSTEREQSLTSLCKRE.....ENAIQSLDGDVTFFGALKIL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1042.5	93.4	285	1 T13B HUMAN	Q9Y275 homo sapien
2	623.5	55.9	309	1 T13B MOUSE	Q9WU72 mus musculus
3	152	13.6	250	1 T13B HUMAN	Q75888 homo sapien
4	143	12.8	241	1 T13B MOUSE	Q9D777 mus musculus
5	91	8.2	1121	1 YJ05 YEAST	P47107 saccharomyc
6	88	7.9	664	1 PRTP HSVB2	P17587 bovine herp
7	87	7.8	4835	1 MDNI_GIALA	Q8T5C1 giardia lam
8	84.5	7.6	637	1 VET HPV35	P27220 human papil
9	84	7.5	591	1 VATA STRP3	Q8K8T1 streptococc
10	82.5	7.4	228	1 LB30 ARATH	O81323 arabidopsis
11	82.5	7.4	737	1 KPCE RAT	P09216 rattus norv
12	82	7.3	233	1 TNFA_LAMGL	P59694 lama glama
13	82	7.3	620	1 GG95 HUMAN	Q08379 homo sapien
14	81.5	7.3	737	1 KPCE MOUSE	P16054 mus musculus
15	81.5	7.3	760	1 CHSX USTMA	Q99126 ustilago ma
16	80.5	7.2	577	1 P2B1 DROME	P48456 drosophila
17	80.5	7.2	2314	1 AKAG RAT	Q9WVC7 rattus norv
18	80	7.2	233	1 TNFA_CANFA	P51742 canis famil
19	79	7.1	233	1 TNFA_TURTR	Q9BEAL tursiops tr
20	78.5	7.0	547	1 ESTA DROPS	P25727 drosophila
21	78	7.0	281	1 COTI HUMAN	Q9BXJ1 homo sapien
22	78	7.0	473	1 C1S1 ARATH	P20115 arabidopsis
23	77.5	6.9	356	1 CMGA BACSU	P25953 bacillus su
24	77.5	6.9	889	1 COPP YEAST	P41811 saccharomyc
25	77.5	6.9	1371	1 UBPU HUMAN	Q94966 homo sapien
26	77	6.9	233	1 TNFA FELCA	P19101 felis silve
27	77	6.9	431	1 STE2 YEAST	P06842 saccharomyc
28	76.5	6.9	555	1 ESTA DROMI	O16168 drosophila
29	76.5	6.9	561	1 KPCE RAT	Q63010 rattus norv
30	76.5	6.9	737	1 KPCE_HUMAN	Q02156 homo sapien
31	76.5	6.9	877	1 WEEL SCHPO	P07527 schizosacch
32	76.5	6.9	968	1 CTDI_HUMAN	O60716 homo sapien
33	76.5	6.9	3214	1 BPAL_HUMAN	Q03001 homo sapien

34 76 6.8 377 1 KAPR_APLCA P31319 aplysia cal
35 76 6.8 1238 1 B3A2_CAVPO Q92088 cavia porce
36 75.5 6.8 510 1 Y0BA_BACSU P45917 bacillus su
37 75.5 6.8 531 1 IMA2_CABEL P12776 caenorhabdi
38 75.5 6.8 548 1 ESTA_DROPE O16173 drosophila
39 75 6.7 233 1 TNFA_DELLE Q8WNR1 delphinapce
40 75 6.7 993 1 TSH DROME P22265 drosophila
41 75 6.7 1042 1 SPAL_HUMAN Q96F84 homo sapien
42 75 6.7 2436 1 ABC2_HUMAN Q9BZC7 homo sapien
43 74.5 6.7 320 1 PR7R_MMTVG P10261 mouse mamma
44 74.5 6.7 324 1 PR7L_MMTVG P03321 mouse mamma
45 74.5 6.7 435 1 YSOI_CABEL Q10127 caenorhabdi

ALIGNMENTS

RESULT 1
T13B_HUMAN
ID T13B HUMAN STANDARD; PRT; 285 AA.
AC Q9Y275;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13B (TNF and APOL-
DE related leukocyte expressed ligand 1) (TALL-1) (B lymphocyte
DE stimulator) (BLYS) (B cell-activating factor) (BAFF) (Dendritic cell-
DE derived TNF-like molecule).
GN TNFSF13B OR TALL1 OR BLYS OR BAFF OR ZTNF4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
[1] SEQUENCE FROM N.A.
RX MEDLINE=99260341; PubMed=10331498;
RA Shu H.-B., Hu W.-H., Johnson H.;
RT "TALL-1 is a novel member of the TNF family that is down-regulated by
RT mitogens";
RL J. Leukoc. Biol. 65:680-683(1999).
RN [2]
[2] SEQUENCE FROM N.A., AND SEQUENCE OF 134-148.
RX MEDLINE=99288033; PubMed=10359578;
RA Schneider P., Mackay F., Steiner V., Hofmann K., Bodmer J.-L.,
RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
RA Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
RA Tschoopp J.;
RT "BAFF, a novel ligand of the tumor necrosis factor family, stimulates
RT B cell growth";
RL J. Exp. Med. 189:1747-1756(1999).
RN [3]
[3] SEQUENCE FROM N.A.
RP TISSUE=Monocytes, and Neutrophils;
RX MEDLINE=99329343; PubMed=10398604;
RA Moore P.A., Belvedere O., Orr A., Pieri K., Lafleur D.W., Feng P.,
RA Soppet D., Charters M., Gentz R., Pamerlee D., Li Y., Galperina O.,
RA Giri J., Roschke V., Nardelli B., Carrell J., Sosnovtseva S.,
RA Greenfield W., Ruben S.M., Olsen H.S., Fikes J., Hilbert D.M.;
RT "Blyys: member of the tumor necrosis factor family and B lymphocyte
RT stimulator";
RL Science 285:260-263(1999).
RN [4]
[4] SEQUENCE FROM N.A.
RP Farrah T., Gross J., Piddington C., O'Hara P.;
RT "Homo sapiens homolog of tumor necrosis factor";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
[5] SEQUENCE FROM N.A.
RP Zhang W., Wan T., Yu Y., Cao X.;
RT "A novel dendritic cell-derived TNF-like molecule";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [6]

Query Match 93.4%; Score 1042.5; DB 1; Length 285;
 Best Local Similarity 76.5%; Pred. No. 2.9e-90;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTERQSLTSCCKREEMKKECVSILPKESPSV-----LLSCC 44
 DB 1 MDDSTERQSLTSCCKREEMKKECVSILPKESPSV-----LLSCC 60

QY 45 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
 DB 61 LTVVSFYQVAALQGLDLSLRAELQGHAEKLPAGA-----KIFEPAP 120

QY 88 GEGNSSQNRKRAVQGPETVTQCLQIADSETPTIQKGYTFVFWLLSPKRGSA-- 145
 DB 121 GEGNSSQNRKRAVQGPETVTQCLQIADSETPTIQKGYTFVFWLLSPKRGSALEE 180

QY 146 -----YGVLYTDKTYANGHLIORKKVVHVGDELSTVLFRCION----- 185
 DB 181 KENKILVKETGYFFTYGVLYTDKTYANGHLIORKKVVHVGDELSTVLFRCIONMPETL 240

QY 186 -----LEEGDELQLAIPRENAQISLDGVTFFGALKLL 218
 DB 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285

RESULT 2
 ID T13B MOUSE STANDARD; PRT; 309 AA.
 AC Q9WU72.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 13B (B cell-activating factor) (BAFF).
 GN TNFSF13B OR BAFF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99288033; PubMed=10359578;
 RA Schneider P., Mackay F., Steiner V., Hofmann K., Bodmer J.-L.,
 RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
 RA Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
 RA Tschopp J.;
 RT "BAFF, a novel ligand of the tumor necrosis factor family, stimulates B cell growth.";
 RT J. Exp. Med. 189:1747-1756(1999).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT SER-79.
 RC STRAIN=NZB.
 RX MEDLINE=21850530; PubMed=11862414;
 RA Jiang Y., Ohtsui M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T.,
 RA Hirose S.;
 RT "Polymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family (Baff) and association with the autoimmune phenotype.";
 RL Immunogenetics 53:810-813(2001).
 CC -!- FUNCTION: Cytokine that binds to TNFSF13B/TACI and TNFSF17/BCMA. TNFSF13/APRIL binds to the same 2 receptors. Together, they form a 2 ligands -2 receptors pathway involved in the stimulation of B- and T-cell function and the regulation of humoral immunity. A third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the survival of mature B-cells and the B-cell response.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
 CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
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 CC -----

DR EMBL; AF119383; AAD22475.1; -
 DR EMBL; AF352245; AAL83939.1; -
 DR MGI; MGI:1344376; Tnfsl3b.
 DR InterPro; IPR006052; TNF_family.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; FALSE NEG.
 DR PROSITE; PS00049; TNF_2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
 KW Polymorphism.
 FT CHAIN 1 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT CHAIN 127 309 MEMBER 13B, MEMBRANE FORM.
 FT CHAIN 127 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 69 309 (POTENTIAL).
 FT SITE 126 127 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 256 269 CLEAVAGE (BY SIMILARITY).
 FT CARBOHYD 117 117 BY SIMILARITY.
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 79 79 N -> S (IN STRAIN NZB).
 SQ SEQUENCE 309 AA; 34192 MW; F3DE6056E6034B4 CRC64;

Query Match 55.9%; Score 623.5; DB 1; Length 309;
 Best Local Similarity 47.4%; Pred. No. 5.5e-51;
 Matches 147; Conservative 24; Mismatches 46; Indels 93; Gaps 7;

QY 1 MDDSTER-EQSLTSCCKREEMKKECVSILPKESPS-----VLLS 42
 DB 1 MDESAKTLPPCLCFCEKSGDMKV-GYDPTTPOKEGAWFGICRDGRLAATLLALLS 59

QY 43 CCLTVSPYQVAALQGLDLSLRAELQGH-----AEKLPAGAKIFEPAPGEGNSS 93

DB 60 SSTFMSLYQVAALQGLDLSLRAELQGH-----AEKLPAGAKIFEPAPGEGNSS 119

QY 94 QNSNRKRAVQGPET-----VTQDCQLIADSET 122
 DB 120 RGHNRRAVQGPETEQVDLSAPAPCLPCRHSQHDNGNMLNIIQDCQLIADSDT 179

QY 123 PTIOKGYTFVFWLLSPKRGSA-----YGVLYTDKTYANGHLIORK 165
 DB 180 PTIRKGYTFVFWLLSPKRGSA-----YGVLYTDKTYANGHLIORK 239

QY 166 KVHVFGDELSLVTLFRCION-----LEEGDELQLAIPRENAQISLDG 208
 DB 240 KVHVFGDELSLVTLFRCIONMPKTLNPNNSCYSAGIARLEEGDELQLAIPRENAQISLRNG 299

QY 209 VTFFGALKLL 218
 DB 300 DTFFGALKLL 309

RESULT 3
 ID TN13 HUMAN STANDARD; PRT; 250 AA.
 AC O75888; Q96HV6; Q9PIM8; Q9PIM9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 43, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-inducing ligand) (APRIL) (TNF-and APOL-related leukocyte expressed ligand 2) (TALL-2) (TNF-related death ligand-1) (TRDL-1).
 GN TNFSF13 OR APRIL OR TALL2 OR ZTNF2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Db 85 EQSDALEAWENGERSRKRRAVLTKQKKQHSLVHLVLPINAT-SKDDSDVTFVWMPALR 143
QY 141 RGSA-----LYGOVLVYDKTYAMGHILQKVVHFGDELSTLFLRCI 183
Db 144 RRGGLQAQGYGVRIQDAGVLYLSQVLFQDVTFTMGQVVSRE-----GQGRQETLFLRCI 197
QY 184 Q-----NLEEGDELQALAIAPRENAQISLDGVDVTFFGALKL 217
Db 198 RSMSPHPRAYNCSYAGVFLHQGDLISVLIIPARAKNLNLSPHGTFLGFKL 250

RESULT 4
TN13 MOUSE
ID TN13 MOUSE STANDARD; PRT; 241 AA.
AC Q9D777; Q9ERP1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-inducing ligand) (APRIL).
GN TNFSF13 OR APRIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=21170294; PubMed=10973284;
RY Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RA "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating humoral immunity";
RT Nat. Immunol. 1:252-256(2000).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RY Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Goshjori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN FUNCTION: Cytokine that binds to TNFSF13B/TACI and to TNFSF17/BCMA. May be implicated in the regulation of tumor cell growth. May be involved in monocyte/macrophage-mediated immunological processes.
RC SUBUNIT: Homotrimer (Potential).
CC -! SUBCELLULAR LOCATION: Secreted (By similarity).
CC -! PTM: The soluble form derives from the membrane form by proteolytic processing.
CC -! SIMILARITY: Belongs to the tumor necrosis factor family.
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CC -----
DR EMBL; AF294825; AAC22534.1; --
DR EMBL; AK009514; BAB26332.1; --
DR MGD; MGI:1916833; Tnfslf13.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR InterPro; IPR006052; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Immune response; Glycoprotein.
FT PROPEP 1 95
FT CHAIN 96 241
FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 13.
FT SITE 95 96
FT DISULFID 187 202
FT CARBOHYD 115 115
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 120 120
SQ SEQUENCE 241 AA; 26889 MW; 4B96D03BDBC712A4 CRC64;
Query Match 12.8%; Score 143; DB 1; Length 241;
Best Local Similarity 26.3%; Pred. No. 3.8e-06;
Matches 56; Conservative 23; Mismatches 68; Indels 66; Gaps 7;
QY 57 QGDLASIRAE---LQGHHAELKLPAGAKIFE-----PPAPGEGNSSQNRKRAVGPPE 107
Db 43 QTELQSLRREVSRVLRQSGSGKQGERPQSLWQSPDVLKAWDKAKSRRRAVLTKGH 102
QY 108 TVTQDCLQI-----ADSETPTIKGSGYTFVPMLLSFKRGSA----- 144
Db 103 KKGSVHLVFPVNTSKADSV-----TEVMQPVLRGRGLEAQGDIVRVWDYGIY 154
QY 145 -LYGOVLVYDKTYAMGHILQKVVHFGDELSTLFLRCI----- 184
Db 155 LLYSQVLFHDVTFMTMGQVVSRE-----GQGRRETFLRCIRSMPSDPDRAYNCSYAGVF 208
QY 185 NLEEGDELQALAIAPRENAQISLDGVDVTFFGALKL 217
Db 209 HLHQGDIITVTKIPRANAKLSLSPHGTFLGFKL 241

RESULT 5
Y109 YEAST
ID Y109 YEAST STANDARD; PRT; 1121 AA.
AC P47107;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hypothetical 127.4 kDa protein in HUL4-GEF1 intergenic region.
GN YJ039W OR J1614.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RL Huang M.-E., Chua J.-C., Galibert F.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Z49538; CAA89566.1; --
DR PIR; S57058; S57058.
DR SGD; S0003800; YJ039W.

RESULT 7

SQ SEQUENCE 591 AA; 64982 MW; 296ACDC372009340 CRC64;
 Query Match 7.5%; Score 84; DB 1; Length 591;
 Best Local Similarity 22.0%; Pred. No. 4;
 Matches 54; Conservative 30; Mismatches 71; Indels 90; Gaps 12;
 QY 1 MDDSTERSQRLTSCCKREEMKCEVSIIPRKES-PSVLLSCCLTVVSYQVAA----- 55
 DB 328 MADSTSRWAEALRENSGLQEM-----PGDEGYPAYLGS---RAEYERAGRVRT 375
 QY 56 -----LQGDLASRLAELOGHAEKLPAGAKIFEPAPGEGNSQNSRNKRAVQGPFEFTV 110
 DB 376 LGSQREGTITAIGA-----VSPPGCDISEP-----VT 403
 QY 111 QDCLOLIA-----DSEPTTIQKSYTFVPWLLSFKRSALYGQVLYTDKTYAMGHLIQRKK- 166
 DB 404 QNTLRIVKFWGLDAPLQRRHFPAINLWTSYS-----LYQDD---VGSYIDRKQE 451
 QY 167 -----VHVFGDELSLVTFRCI--QNLREGDELQALPR-----ENAIQLSD 206
 DB 452 SNWSNKVTRMAILOREASLEIVLVGLDLSLSEQDRLTMVARQIREYDLYQNAFDSVD 511
 QY 207 GDVTF 211
 DB 512 TFSF 516

RESULT 10

ID LB30 ARATH STANDARD; PRT; 228 AA.
 AC 081323;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE LOB domain protein 30.
 GN LB30 OR AT4G00220 OR FGN15.4.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RC SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
 RP STRAIN=cv. Columbia;
 RX MEDLINE=22063719; PubMed=12068116;
 RA Shuai B., Reynaga-Pena C.G., Springer P.S.;
 RT "The LATERAL ORGAN BOUNDARIES Gene defines a novel, plant-specific
 RL gene family."
 RL Plant Physiol. 129:747-761(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,
 RA Kreis M., Deiseny M., Puigdomenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirks W.,
 RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA De Keyser A., Buysschaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., Mclay K., Mayes R.,
 RA Pettett A., Rajandream M.A., Lyne M., Rees V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehnert T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
 RA Massenet O., Quigley P., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chedford F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,
 RA Friselman D., Haase D., Lencke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threiden J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spiech J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antonoli B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
 RA Chen E., Marra M., Martienssen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana."
 RL Nature 402:769-777(1999).
 CC -!- TISSUE SPECIFICITY: Expressed in roots, stems, leaves and flowers.
 CC -!- SIMILARITY: Contains 1 LOB domain.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AF432232; AAL27613.1; -;
 DR EMBL; AF069229; AAC19300.1; -;
 DR EMBL; AL461471; CAB80780.1; -;
 DR FIR; T01350; T01350.
 DR InterPro; IPR004883; DUF260.
 DR Pfam; PF03195; DUF260; 1.
 DR PROSITE; PS50891; LOB; 1.
 FT DOMAIN 16 118
 LOB
 SQ SEQUENCE 228 AA; 23968 MW; CAE3F2DA4C78A209 CRC64;
 Query Match 7.4%; Score 82.5; DB 1; Length 228;
 Best Local Similarity 25.1%; Pred. No. 1.6;
 Matches 46; Conservative 23; Mismatches 63; Indels 51; Gaps 9;
 QY 18 KREEMKCEVSIIPRKESPSVLLSCCLTVVSYF-YQVAAOGLASRLAELOGHAEKLP 76
 DB 70 KRPAVVSICFEAQARLRDP--IYGCVSHVSLVQVQVVSQVLSYLAQHL----- 118
 QY 77 AGAKIFPPAPGEGNSQNSRNKRAVQGPFEFTVTDCLQLIADSETPTIQKSYTFVFWL 136
 DB 119 ATLEPQPPQPPVPSVSGS-----LQALSIDLPTISVVDL----- 157
 QY 137 LSPKRSALYQGVLYTDKTYAMGHLIQRKKVHVFGDELSTVTLFRCLONLEGBELQAL 196
 DB 158 -----SSIEPEVNV--SSTWAMQQQ-PRPSDHLFGVPSS-----SNMGGGGELQ-AL 199
 QY 197 PRE 199
 DB 200 ARE 202
 RESULT 11
 KPCE_RAT
 ID KPCE_RAT
 AC P09216;
 DT 01-MAR-1989 (Rel. 10, Created) PRT; 737 AA.

FT	NP BIND	414	422	ATP (BY SIMILARITY).
FT	BINDING	437		ATP (BY SIMILARITY).
FT	ACT SITE	532		BY SIMILARITY.
FT	MOD_RES	703		PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	MOD_RES	710		PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	SEQUENCE	737 AA;	83478 MW;	6AD6999EFDD2659F CRC64;

Query Match 7.4%; Score 82.5; DB 1; Length 737;
 Best Local Similarity 20.7%; Pred. No. 7.3;
 Matches 50; Conservative 34; Mismatches 88; Indels 69; Gaps 10

QY	19	REEMKLKCVSILPRKSPSVLLSCCLTVVSVFQVALQGLDASLRAEL--QGHHAELKLP	76
DB	268	ROGLQCKVCKMNVHRCETNAPNC---GVDARGIAKVLADLGVTPDKITNSGQRRKKLA	324
QY	77	AGAKIFEPPAPGEGNS--SONSRNKRAVQGP-----EETVTQDC	113
DB	325	AGA---ESPQSPAGNSPESDDRKSATSPSCDQELKELENNRKALSFNRRGEEHRASS	381
QY	114	L--QLIADSEFTTIQKG-----SYTFVPWLLSFKRGSAHYGVQLYTDKTYAMGHLIQ	163
DB	382	TDGQLASPGENGVEVRQGAKEGLGIDENFIKVLGKSGFGKVMLELKGDEVYAV--KVL	439
QY	164	RKKVIVFGDELS-----LVTLFRCIQNL-----EGDELQALTP	197
DB	440	KDVTILODDVDVCTMTKEKILARLKHPLYLTOLYCCFOTKDRLFFVMEVYVNGDGLMFQIQ	499
QY	198	R 198	
DB	500	R 500	

RESULT 12
 TNFA_LAMGL STANDARD; PRT; 233 AA.

ID	TNFA_LAMGL	STANDARD;	PRT;	233 AA.
AC	P59694;			
DT	15-SEP-2003 (Rel. 42, Created)			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor			
DE	ligand superfamily member 2) (TNF-a) (Cachectin).			
DE	TNF OR TNFSF2 OR TNFA.			
OS	Lama glama (Llama).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.			
OX	NCBI_TaxID=9844;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Raadon O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,			
RA	Onuma M.;			
RT	"Cloning and sequence analysis of cytokine cDNAs of llama and camel.;"			
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and			
CC	TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can			
CC	induce cell death of certain tumor cell lines. It is potent			
CC	pyrogen causing fever by direct action or by stimulation of			
CC	interleukin 1 secretion and is implicated in the induction of			
CC	cachexia. Under certain conditions it can stimulate cell			
CC	proliferation and induce cell differentiation (By similarity).			
CC	-!- SUBUNIT: Homotrimer (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an			
CC	extracellular soluble form (By similarity).			
CC	-!- PTM: The soluble form derives from the membrane form by			
CC	proteolytic processing (By similarity).			
CC	-!- PTM: The membrane form, but not the soluble form, is			
CC	phosphorylated on serine residues. Dephosphorylation of the			
CC	membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By			
CC	similarity).			
CC	-!- SIMILARITY: Belongs to the tumor necrosis factor family.			

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CC EMBL; AB107646; BAC75383.1; -
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS0049; TNF 2; 1.
CC Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
CC CHAIN 1 233
FT CHAIN 77 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM (BY
FT CHAIN 77 233 SIMILARITY).
FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM (BY
FT CHAIN 77 233 SIMILARITY).
FT DOMAIN 1 34 CYTOSOLIC (POTENTIAL).
FT TRANSMEM 35 57 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT TRANSMEM 35 57 (BY SIMILARITY).
FT DOMAIN 58 233 EXTRACELLULAR (POTENTIAL).
FT MOD RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25437 MW; F5C07837505PBD86 CRC64;

Query Match 7.3%; Score 82; DB 1; Length 233;
Best Local Similarity 22.5%; Pred. No. 1.9;
Matches 52; Conservative 29; Mismatches 92; Indels 58; Gaps 9;
QY 31 LPRKE-SPSVLLSC-CLTVSVFYQVAALQGDLSRAELQGHAKLPAGAKIPEPPAPG 88
DB 17 LPKAGGQGGRRCCULSFLVAGATTFLCLHFGVIGPQKEELTGQIWNPLAQT 76
QY 89 EGNSSQNRKRAVQGPETVTQDCLQ-----LIA-----DSEPTTIQKGSYTFVP 134
DB 77 LRSSQASRDVPAHVADPAAQQLQWEKRPANLLANGVKLEDNQLVVPDGLY---- 132
QY 135 WLLSPKRSALYGVLYTDK-----TYANGHLIQKKVHVGDELSVTLFR--C----- 182
DB 133 -----LIYSQVLFSGRCPCSTFVFLTHITISLAVS--YFNKANLSAINKSPCQGGTS 182
QY 183 -----IQNLEGDELOLAIPRENAQISLDGVTVPFGALKL 217
DB 183 EBAEAKPWYPIYLGGVFQLEKDDRLSAEINPNVYLDFAESGVVFGIAL 233

RESULT 13
GG95_HUMAN
ID GG95_HUMAN STANDARD; PRT; 620 AA.
AC Q08379;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Golgin-95.
GN GOLGA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93301617; PubMed=8315394;
RA Fritzler M.J., Hamel J.C., Ochs R.L., Chan E.K.L.;
RT "Molecular characterization of two human autoantigens; unique cDNAs
RT encoding 95- and 160-kD proteins of a putative family in the Golgi
RT complex.";
RL J. Exp. Med. 178:49-62(1993).
CC -!- FUNCTION: GOLGI AUTO-ANTIGEN; MAY HAVE A FUNCTION IN THE
CC PROCESSING AND TRANSPORT OF PROTEINS THROUGH THE GOLGI.
CC -!- DOMAIN: EXTENDED ROD-LIKE PROTEIN WITH COILED-COIL DOMAINS.
CC -!- SIMILARITY: HIGH, TO RAT CIS-GOLGI MATRIX PROTEIN GML30.
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CC EMBL; L06147; AAA35920.1; -
CC PIR; JH0821; JH0821.
CC Genew; HGNC:4425; GOLGA2.
CC MIM; 602580; -
CC GO; GO:0005794; C:Golgi apparatus; TAS.
KW Golgi stack; Coiled coil.
FT DOMAIN 5 336 COILED COIL (POTENTIAL).
FT DOMAIN 352 510 COILED COIL (POTENTIAL).
FT DOMAIN 67 73 POLY-GLU.
FT DOMAIN 322 333 POLY-GLU.
SQ SEQUENCE 620 AA; 70472 MW; 54B31A0FB42BFC8 CRC64;

Query Match 7.3%; Score 82; DB 1; Length 620;
Best Local Similarity 25.2%; Pred. No. 6.6;
Matches 41; Conservative 20; Mismatches 52; Indels 50; Gaps 7;
QY 3 DSTERQSLTSCCLKKEEMKKECVSILPKESPSVLLSCCLTVWGFYQ--VAALQDGL 60
DB 317 DGLDRE-----EEDDEEEEAVALPQPMSPIDEDLESREANVAFFNSAVASAEQ 369
QY 61 ASLRAELQGH-----AEKLPAKAKIPEPPAPGEGNSSQNRKRAVQGP--- 105
DB 370 ARLAQKQEVRCRRRLAHLASAKPEAA---APAGTGGDSVCGCTHRLQGA MEK 425
QY 106 -----EETVQDCLQIADSETPTIQKSY 130
DB 426 LQSRFMELOEKADLKERVELEHRCIQL--SGETDTI--GEY 464

RESULT 14
KPCE_MOUSE
ID KPCE_MOUSE STANDARD; PRT; 737 AA.
AC P16054;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
GN PKCE OR PKCE OR PKCEA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89137541; PubMed=2917656;
RA Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
RT "Unique substrate specificity and regulatory properties of
RT PKC-epsilon: a rationale for diversity.";
RL FEBS Lett. 243:351-357(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98127436; PubMed=9467942;
RA Wang Q.J., Acs P., Goodnight J., Blumberg P.M., Mischak H.,
RA Mushinski J.F.;
RT "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and -
RT epsilon chimeras, is responsible for conferring tumorigenicity to
RT NIH3T3 cells, whereas both regulatory and catalytic domains of
RT PKC-epsilon contribute to in vitro transformation.";
RL Oncogene 16:53-60(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Wheeler D.L.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN

PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
-|- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
binding domains.
-|- SIMILARITY: Contains 1 C2 domain.
-|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
PKC SUBFAMILY.

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EMBL; AF028009; AAB84189.1; --
EMBL; AF325507; AAG53692.1; --
PIR; S02270; KIMSCE.
HSSP; P28867; IPTQ.
MGI; MGI:97599; Pkckc.
GO; GO:0004699; F.calcium independent protein kinase C activity; IDA.

InterPro; IPR000008; C2.
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000961; Pkinase C.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.

Pfam; PF00168; C2; 1.
Pfam; PF00130; DAG_PE-bind; 2.
Pfam; PF00069; pkinase; 1.
Pfam; PF00433; pkinase C; 1.
PRINTS; PRO0008; DAGPEDOMAIN.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00109; C1; 2.
SMART; SM00239; C2; 1.
SMART; SM00133; S_TK_X; 1.
SMART; SM00220; S_TK; 1.

PROSITE; PS00004; C2 DOMAIN 2; 1.
PROSITE; PS00479; DAG PE BIND DOM 1; 2.
PROSITE; PS00081; DAG PE BIND DOM 2; 2.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00111; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.

FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 408 668 PROTEIN KINASE.

FT NP_BIND 414 422 ATP (BY SIMILARITY).
FT BINDING 437 437 ATP (BY SIMILARITY).
FT ACT_SITE 532 532 BY SIMILARITY.
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 737 AA; 83560 MW; 7AEBB8CC10C99F57 CRC64;

Query Match 7.3%; Score 81.5; DB 1; Length 737;
Best Local Similarity 20.7%; Pred. No. 9.1;
Matches 50; Conservative 33; Mismatches 89; Indels 69; Gaps 10;

QY 19 REEMKLEKCVSLIPKSPSVLLSCCLTVVSFYQVAALQGLDASLRAEL--QGHAELKIP 76
Db 268 RQLQCKVKCMNVHRRCTENAPNC---GVDARGIAKVLADLGVTDPKITNSGQRKKLA 324
QY 77 AGAKIFPPAPAGEGNS-SQNSRNKRAVQCP-----EETVQDC 113
Db 325 AGA---ESPQASGNSPDSRDSKAPTSPCDQLKELENNIRKALSFDRNGEEHRASSA 381
QY 114 L--QLIADSETTIQKG-----SYTFVPMLSKFGSALYGVLYTDKTYAMGHLIQ 163
Db 382 TDGQLASPGENGSEVRPGQAKRLGLDGFNFIKVLKSGSGFKGVMIAELKKGDEYAV--KVL 439
QY 164 RKKVHVFGDEL-----LVTLFRCIQNL-----EGDELQALIP 197

Db 440 KKDVLQDDVDCTMTKRIILALARKHPYLQLYCCFQTKDRLFFVMEYVNGDLMFQIQ 499
QY 198 R 198
Db 500 R 500

RESULT 15

CHSX_USTMA

ID CHSX_USTMA STANDARD; PRT; 760 AA.

AC Q99126;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Chitin synthase 1 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl
transferase 1).

DE CHS1.

OS Ustilago maydis (Smut fungus).

OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;

OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

OX NCBI_TaxID=5270;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RK32 / A2B3;

RX MEDLINE=97086517; PubMed=8932711;

RA Xocoostle-Cazares B., Leon-Ramirez C., Ruiz-Herrera J.;

RT "Two chitin synthase genes from Ustilago maydis.";

RL Microbiology 142:377-387(1996).

CC -|- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.

CC -|- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + (1,4)-(N-acetyl-

CC beta-D-glucosaminyl) (N) = UDP + (1,4)-(N-acetyl-beta-D-

CC glucosaminyl) (N+1).

CC -|- SUBCELLULAR LOCATION: Plasma membrane-bound.

CC -|- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.

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EMBL; X87748; CAB61027.1; --

PIR; S55520; S55520.

InterPro; IPR004834; Chitin synth.

Pfam; PF01644; Chitin synth; 1.

ProDom; PD002998; Chitin synth; 1.

KW Transferase; Glycosyltransferase; Transmembrane; Cell wall;

KW Multigene family.

SQ SEQUENCE 760 AA; 85181 MW; 9377000F57410993 CRC64;

Query Match

Best Local Similarity 7.3%; Score 81.5; DB 1; Length 760;

Matches 39; Conservative 33; Mismatches 59; Indels 55; Gaps 8;

QY 85 PAPERGNSQNSRNKRAVQ-----GPEETVQDCQLIADSETPIQKSYTFVPWL 136
Db 236 PAPERGAQRHRTKKNVRLTKKPHSGLPVTKLTQTLFTRRAEDFTTMRYSAVTCDPTD 285
QY 137 L--SPKRGSAALYGO-----VLYTD-----KTY-----AMGHLIQRKKVHVFGDE-- 173
Db 286 LERFETLPPALYGRHTELFIAITWNEDEVLCFTFHGVMKNIAHLCSRNKSRTWKGKDW 345
QY 174 ----LSLVT-----LFRCI-----ONLEGEDELQALIPRENAQISLDGVD 209
Db 346 KKVVAIISDCRKKIHPRVLDCLAAALGVYQGVAKNMVDGKVRHAHLYEYTTQLSDSNL 405
QY 210 TFFGA 214
Db 406 QFKGA 410

Search completed: February 3, 2004, 07:44:14
Job time : 12.2044 secs

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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 29.0667 Seconds
(without alignments)
1935.395 Million cell updates/sec

Title: US-09-911-777-1

Perfect score: 1116

Sequence: 1 MDDSTERQSLTSLCKRE.....ENAIQLSDGVDVTFGALKLL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	750.5	67.2	208	Q8IZI6	Q8IZI6 homo sapien
2	677	60.7	174	Q8IZI5	Q8IZI5 homo sapien
3	610	54.7	258	Q8BZM8	Q8BZM8 mus musculus
4	596	53.4	158	Q8IZI4	Q8IZI4 homo sapien
5	497.5	44.6	288	Q8JHJ4	Q8JHJ4 gallus gall
6	252.5	22.6	199	Q8BWP2	Q8BWP2 mus musculus
7	249.5	22.4	194	Q8BVA3	Q8BVA3 mus musculus
8	152	13.6	250	Q8NFH7	Q8NFH7 homo sapien
9	146	13.1	410	Q8BX52	Q8BX52 mus musculus
10	140.5	12.6	330	Q8IZK7	Q8IZK7 homo sapien
11	91.5	8.2	267	Q8B67	Q8B67 rhizobium 1
12	91.5	8.2	695	Q8W2R3	Q8W2R3 oryza sativ
13	88	7.9	1746	Q8AXN0	Q8AXN0 glaucosphae
14	87.5	7.8	240	Q55896	Q55896 synechocyst
15	87.5	7.8	748	Q8W0N1	Q8W0N1 oryza sativ
16	87.5	7.8	1524	Q8RYN2	Q8RYN2 oryza sativ

ALIGNMENTS

RESULT 1

Q8IZI6 PRELIMINARY; PRT; 208 AA.

AC Q8IZI6;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE B-lymphocyte stimulator (Fragment).
GN TNFSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gao H., He F., Li R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129226; AN08422.1; -
FT NON_TER
SQ SEQUENCE 208 AA; 22767 MW; EEA31D227033AA53 CRC64;

Query Match 67.2%; Score 750.5; DB 4; Length 208;
Best Local Similarity 75.0%; Pred. No. 6e-69;
Matches 156; Conservative 0; Mismatches 1; Indels 51; Gaps 3;
QY 62 SLRAELQGHAEKLPAGA-----KIFPPAPGEGNSQNSRNKRAVQG 104
DB 1 SLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFPPAPGEGNSQNSRNKRAVQG 60
QY 105 PEETVTQDCLQIADSETPTIOKGSYTFVPWLLSKFGKGSAL-----YG 147
DB 61 PEETVTQDCLQIADSETPTIOKGSYTFVPWLLSKFGKGSAL-----LESGD 120
QY 148 QLVYTDKTYANGHLIQKKVHVFGEISLVTLFRICQN-----LESGD 190
DB 121 QLVYTDKTYANGHLIQKKVHVFGEISLVTLFRICQN-----LESGD 180
QY 191 ELQALAIAPRENAQISLDGVDVTFGALKLL 218

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Db 181 ELQLTIPRENAQISLDGVDVTFPGALKLL 208
RESULT 2
Q81Z15 PRELIMINARY; PRT; 174 AA.
AC Q81Z15;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE B-lymphocyte stimulator (Fragment).
GN TNFSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129227; AAN08423.1; -.
FT NON_TER
SQ SEQUENCE 174 AA; 19479 MW; 1AEBD4F2862EB3E0 CRC64;

Query Match 60.7%; Score 677; DB 4; Length 174;
Best Local Similarity 79.8%; Pred. No. 1.7e-61;
Matches 138; Conservative 0; Mismatches 1; Indels 34; Gaps 2;

Qy 80 KIFEPAPGEGNSQNSNRKRAVQPEETVQDCQLIADSETPTIQKGSYTFVPWLLSF 139
Db 2 KIFEPAPGEGNSQNSNRKRAVQPEETVQDCQLIADSETPTIQKGSYTFVPWLLSF 61
Qy 140 KRGSL-----YQVLYTDKTYAMGHLIQRKKVHVFGEDELSTVTLFRC 182
Db 62 KRGSALEKENKILVKTGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGEDELSTVTLFRC 121
Qy 183 IQN-----LEEGDELOLAIPRENAQISLDGVDVTFPGALKLL 218
Db 122 IQNPETLPNNSCYSAGIAKLEEGDELQITIPRENAQISLDGVDVTFPGALKLL 174

RESULT 3
Q8BZM8 PRELIMINARY; PRT; 258 AA.
AC Q8BZM8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Tumor necrosis factor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RL STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12468851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK034121; BAC28593.1; -.
FT NON_TER
SQ SEQUENCE 258 AA; 28604 MW; E6431FE93E782810 CRC64;

Query Match 54.7%; Score 610; DB 11; Length 258;
Best Local Similarity 53.0%; Pred. No. 2.3e-54;
Matches 134; Conservative 17; Mismatches 28; Indels 74; Gaps 4;

Qy 40 LLSCLTIVSYFQVAALQGDLASLRAELQGH-----AEKLPAGAKIFEPAPGEG 90
Db 6 LLSSTFTAMSLYQLAALQADLMNLRLWELQSYRGSAATPAAGAPELTAGVKLLTPAAPRPH 65

Qy 91 NSSQNSNRKRAVQPEET-----VTQDCQLIAD 119
Db 66 NSSRGRNRRAFAVQPEETQDVLSAPPAPCLPCRHSQDDNGMNLNRNIQDCQLIAD 125
Qy 120 SETPTIQKGSYTFVPWLLSFKRGSL-----YQVLYTDKTYAMGHLI 162
Db 126 SDFTIRKGYTFVPWLLSFKRGNALEKENKIVVRQTGYFFIYQVLYTDPIFAMGHVI 185
Qy 163 QRKKVHVFGEDELSTVTLFRCIQN-----LEEGDELOLAIPRENAQISL 205
Db 186 QRKKVHVFGEDELSTVTLFRCIQNMPTLPNNSCYSAGIARLEEGDEIQLAIPRENAQISR 245
Qy 206 DGDVTFPGALKLL 218
Db 246 NGDDTFFGALKLL 258

RESULT 4
Q81Z14 PRELIMINARY; PRT; 158 AA.
AC Q81Z14;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE B-lymphocyte stimulator (Fragment).
GN TNFSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL He F., Gao H., Li R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129228; AAN08424.1; -.
FT NON_TER
SQ SEQUENCE 158 AA; 17826 MW; 8346BCC0D333DCAB CRC64;

Query Match 53.4%; Score 596; DB 4; Length 158;
Best Local Similarity 77.8%; Pred. No. 3.2e-53;
Matches 123; Conservative 0; Mismatches 1; Indels 34; Gaps 2;

Qy 95 NSNRKRAVQPEETVQDCQLIADSETPTIQKGSYTFVPWLLSFKRGSL----- 145
Db 1 NSNRKRAVQPEETVQDCQLIADSETPTIQKGSYTFVPWLLSFKRGSALEKENKILV 60
Qy 146 -----YQVLYTDKTYAMGHLIQRKKVHVFGEDELSTVTLFRCIQN----- 185
Db 61 KETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGEDELSTVTLFRCIQNMPTLPNNSCYS 120
Qy 186 -----LEEGDELOLAIPRENAQISLDGVDVTFPGALKLL 218
Db 121 AGIAKLEEGDELOLTIIPRENAQISLDGVDVTFPGALKLL 158

RESULT 5
Q8JHJ4 PRELIMINARY; PRT; 288 AA.
AC Q8JHJ4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE TNF family B cell activation factor.
GN BAFF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RL Schneider K., Koltow S., Schneider P., Goebel T., Kaspers B.,
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Db          180 PIRKGS 186
||||:||||
RESULT 7
QBVA3
ID QBVA3 PRELIMINARY; PRT; 194 AA.
AC QBVA3;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Tumor necrosis factor.
DE Mus musculus (Mouse)
OS
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RC MEDLINE=22354683; PubMed=12466851;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RT Nature 420:563-573 (2002).
RL EMBL; AK079180; BAC37571.1; -.
DR SEQUENCE 194 AA; 20961 MW; 85PCF3495B138377 CRC64;
SQ
Query Match 22.4%; Score 249.5; DB 11; Length 194;
Best Local Similarity 36.4%; Pred. No. 1.9e-17;
Matches 68; Conservative 19; Mismatches 41; Indels 59; Gaps 5;
QY 1 MDDSTER-EQSRLTSLCKREEMKKECVSILPRKESPS-----VLLS 42
DB 1 MDESATLPPCLCFCEKGEDMKV-GYDPITQKEGAWFGICRDGRLAATLLALLS 59
QY 43 CCLTVVSFTYQVAALQGDLASLRAELQGH-----ABKLPAGAKIFPPAPGEGNSS 93
DB 60 SGTAMSLYQLAALQADLNLRLMELQSYRGSAATPAAAGAPELTAGVKLLTPAAPRPINSS 119
QY 94 QNSRKNRAVQGPET-----VTQCLQLIADSET 122
DB 120 RGHNRRAFCQGPETEQQVDLSAPPAPCLPGCRHSQHDNGMNLNIIQDCLQLIADSDT 179
QY 123 PTIOKGS 129
DB 180 PIRKGN 186
||||:||||
RESULT 8
QB8FH7
ID QB8FH7 PRELIMINARY; PRT; 250 AA.
AC QB8FH7;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Proliferation-inducing ligand APRIL.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Koyama T., Tsukamoto H., Masumoto K., Himeji D., Hayashi K.,
RA Harada M., Horluchi T.;
RA "Genomic structure of APRIL, a proliferation-inducing ligand.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF513501; AA047279.1; -.
DR InterPro; IPR006052; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.

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SQ SEQUENCE 250 AA; 27453 MW; AE1E4FDEFD578898 CRC64;
Query Match 13.6%; Score 152; DB 4; Length 250;
Best Local Similarity 24.9%; Pred. No. 2.8e-07;
Matches 58; Conservative 31; Mismatches 64; Indels 80; Gaps 9;

QY 41 LSCCLTVVSYQVAALQGDLSARAE---LQGHAEKLPAGAKIPEPPAPGEG----- 90
DB 42 VACAWALIT-----QQTELQSLREVSRLOQ-----TGG-----PSQNGEGYPWQSLP 84
QY 91 -----NSSQNRKRAVQGPETVTQDCLQLIADSETPTTQKGSYTFVPWLLSFK 140
DB 85 EQSSDALEAWENGERSRKRRAVLTKQKKQHSVLHVPINAT-SKDDSDVTEVMQPALR 143
QY 141 RGSAA-----LYGOVLYTDKTYANGHLIQRKXHVFGDELSTLFRCI 183
DB 144 RGRGLQAQGYGVRIQDAGVYLLSQVLFQDVTFTMGQVVSRE-----GQGRQETLFRCI 197
QY 184 O-----NLEEGDELQALIPRENAQISLDGDVTFPGALKL 217
DB 198 RSMPSHPDRAYNCYSAGVFHLHQGDILSVIIPRARKLNLSPHGTFLGFVKL 250

RESULT 9
QBX52
ID Q8BX52 PRELIMINARY; PRT; 410 AA.
AC Q8BX52;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tumor necrosis factor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK044387; BAC31897.1; --
SQ SEQUENCE 410 AA; 45881 MW; 590A4B74C33FB8D4 CRC64;

Query Match 13.1%; Score 146; DB 11; Length 410;
Best Local Similarity 26.1%; Pred. No. 2.3e-06;
Matches 57; Conservative 24; Mismatches 71; Indels 66; Gaps 7;

QY 52 QVAALQGDLSARAE---LQGHAEKLPAGAKIFE-----PPAPGEGNSSQNRKRAV 102
DB 207 QLRLCQTELQSLREVSRVLRSGSPQKQGERPQWQSLMEQSDVLEAKWDGAKSRRRRAV 266
QY 103 QGPETVTQDCLQLI-----ADSETPTTQKGSYTFVPWLLSFKRGA----- 144
DB 267 LTQHKHKKHSHVHLVFNITSKADSDV-----TEVMQVLRGRGLEAQGDIVRW 318
QY 145 -----LYGOVLYTDKTYANGHLIQRKXHVFGDELSTLFRCIQ----- 184
DB 319 DTGIVYLLYSQVLFHDVTFMTMGQVVSRE-----GQGRRETLCIRSMPSDPDRAYNSCY 372
QY 185 -----NLEEGDELQALIPRENAQISLDGDVTFPGALKL 217
DB 373 SAGVFHLHQGDIIITVKIPRANKLSLSPHGTFLGFVKL 410

RESULT 10
Q81ZK7
ID Q81ZK7 PRELIMINARY; PRT; 330 AA.
AC Q81ZK7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
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DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE TWE-PRIL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22299924; PubMed=12411489;
RA Prader-Balade B.; Medema J.P.; Lopez-Fraga M.; Lozano J.C.;
RA Kolfshoten G.M.; Picard A.; Martinez-A C.; Garcia-Sanz J.A.;
RA Hahne M.;
RT "An endogenous hybrid mRNA encodes TWE-PRIL, a functional cell surface
RT TWEAK-APRIL fusion protein."
RL EMBL J. 21:5711-5720 (2002).
DR EMBL; AY081051; AAL90443.1; --
SQ SEQUENCE 330 AA; 36588 MW; FC6F3BCA29C029AE CRC64;

Query Match 12.6%; Score 140.5; DB 4; Length 330;
Best Local Similarity 26.5%; Pred. No. 6.3e-06;
Matches 43; Conservative 24; Mismatches 52; Indels 43; Gaps 4;

QY 92 SSQNRKRAVQGPETVTQDCLQLIADSETPTTQKGSYTFVPWLLSFKRGA----- 144
DB 176 NGRSRKRRAVLTKQKKQHSVLHVPINAT-SKDDSDVTEVMQPALRRGRGLQAQGYG 234
QY 145 -----LYGOVLYTDKTYANGHLIQRKXHVFGDELSTLFRCIQ----- 184
DB 235 VRIQDAGVYLLSQVLFQDVTFTMGQVVSRE-----GQGRQETLCIRSMPSHPDRAY 288
QY 185 -----NLEEGDELQALIPRENAQISLDGDVTFPGALKL 217
DB 289 NSCVSAGVFHLHQGDILSVIIPRARKLNLSPHGTFLGFVKL 330

RESULT 11
Q98B67
ID Q98B67 PRELIMINARY; PRT; 267 AA.
AC Q98B67;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Transcriptional regulator.
GN MLL5707.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T.; Nakamura Y.; Sato S.; Asamizu E.; Kato T.; Sasamoto S.;
RA Watanabe A.; Idekawa K.; Ishikawa A.; Kawashima K.; Kimura T.;
RA Kishida Y.; Kiyokawa C.; Kohara M.; Matsumoto M.; Mateuno A.;
RA Mochizuki Y.; Nakayama S.; Nakazaki N.; Shimo S.; Sugimoto M.;
RA Takeuchi C.; Yamada M.; Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338 (2000).
DR EMBL; AP003007; BAB52105.1; --
DR InterPro; IPR001034; HTH_Deor.
DR Pfam; PF00455; deor; 1.
DR PRINTS; PR00037; HTHLACR.
DR SMART; SM00420; HTH_DEOR; 1.
DR PROSITE; PS00894; HTH_DEOR_FAMILY; 1.
KW Complete proteome.
SQ SEQUENCE 267 AA; 29577 MW; 03E99717CA35F544 CRC64;

Query Match 8.2%; Score 91.5; DB 16; Length 267;
Best Local Similarity 21.2%; Pred. No. 0.51;
Matches 48; Conservative 39; Mismatches 70; Indels 69; Gaps 11;
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QY 6 EREQSR-LTSCLKREEMKKECVSLPKESPSVLLSCCLTVWSFYQVAALQGLASLR 64
Db 3 EKERHRIILSAVQEPVTVQEWDLTSESSE-----ATIRRDIAALH 44
QY 65 AELQGHAEKLPAGAKIFEP-----APGSGNSSQNRKRAVQGPETVTQDCLQI 117
Db 45 VQ---KRLRVRGGAETSPPOFIGLAGRPFSVNETINASKRA-----IAREAVEIC 94
QY 118 ADSEPTTQKGSYTFVPMLLSKFGSALYGVLYTDKTYAMGHLIQRKXVHVFGDELSIV 177
Db 95 GGEPIIINGGTTT---QVHLELTGRM---PFTNSPFIAPHLKHSKNTVM---LSGG 146
QY 178 TLFRCTQNLQEGDELQALPENAQIS-LDGDVT-----FFGA 214
Db 147 TIYR-----EQNIILSPDNDVTRNFYARRFMGA 176

RESULT 12
QW2R3
ID Q8W2R3 PRELIMINARY; PRT; 695 AA.
AC Q8W2R3;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Putative wall-associated protein kinase.
GN OSJNBA0028C16.9.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A.; Yu Y.; Soderlund C.; Chen M.; Kim H.-R.; Rambo T.;
RA Saski C.; Henry D.; Oates R.; Simmons J.;
RT "Rice Genomic Sequence.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC098565; RAL69427.1; -.
DR Gramene; Q8W2R3; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; EGF-like domain; Kinase; Transferase.
SQ SEQUENCE 695 AA; 77048 MW; D9DEFE3A74A655A5 CRC64;

Query Match 8.2%; Score 91.5; DB 10; Length 695;
Best Local Similarity 27.4%; Pred. No. 1.9;
Matches 46; Conservative 26; Mismatches 77; Indels 19; Gaps 9;

QY 40 LLSCCLTV---VSFYQVAALQGLASLRAELQGHAEKLPAGAKIFEPAPGEGNSSQNS 96
Db 479 LLGCLLEVDVPMVLYEFAA-KGNLQDI---LHGDNIPPLGLRLNIAESAEGLRYMHS 534
QY 97 RNKRAVQGPETVTQDCLQIADSETPTTQKGSYTFVPMLLSKFGSALY---GVLYTDK 154
Db 535 STSRTIRHGD---VRPANILLTDKTIPTKI---SYFGTSKLLTVDKDFTFVVGSMGYIDP 588
QY 155 TY-AMGHLIQRKXVHVFGDELSIVTLFRCTQNLQEGDELQALPENA 201
Db 589 VFHKTGHLTKQSDVSFG---VWLELI-CRKPTIYGENCSLIIIEFQNA 633

RESULT 13
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Q9AXN0
ID Q9AXN0 PRELIMINARY; PRT; 1746 AA.
AC Q9AXN0;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE DNA-dependent RNA polymerase II largest subunit RPB1.
GN RPB1.
OS Glaucosphaera vacuolata.
OC Eukaryota; Glaucocystophyceae; Gloeochaetales; Glaucosphaeraeae;
OC Glaucosphaera.
OX NCBI_TaxID=38265;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21336853; PubMed=11443356;
RA Stiller J.W.; Riley J.; Hall B.D.;
RT "Are red algae plants? A critical evaluation of three key molecular
RT data sets.";
RL J. Mol. Evol. 52:527-539 (2001).
DR EMBL; AF315820; AAK00310.1; -.
DR InterPro; IPR002965; P rich exten.
DR InterPro; IPR006592; RNA_pol_A_N.
DR InterPro; IPR000684; RNA_polII_repeat.
DR InterPro; IPR000722; RNA_pol_A.
DR InterPro; IPR007080; RNA_pol_Rpb1_1.
DR InterPro; IPR007066; RNA_pol_Rpb1_3.
DR InterPro; IPR007083; RNA_pol_Rpb1_4.
DR InterPro; IPR007081; RNA_pol_Rpb1_5.
DR InterPro; IPR007075; RNA_pol_Rpb1_6.
DR InterPro; IPR007073; RNA_pol_Rpb1_7.
DR Pfam; PF04997; RNA_pol_Rpb1_1; 1.
DR Pfam; PF00623; RNA_pol_Rpb1_2; 1.
DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.
DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.
DR Pfam; PF04998; RNA_pol_Rpb1_5; 1.
DR Pfam; PF04992; RNA_pol_Rpb1_6; 1.
DR Pfam; PF04990; RNA_pol_Rpb1_7; 1.
DR PRINTS; PR01217; PRICHEXTENSN.
DR SMART; SM00663; RPOA_N; 1.
DR PROSITE; PS00115; RNA_POL_II_REPEAT; 12.
DR PROSITE; PS00115; RNA_POL_II_REPEAT; 12.
SQ SEQUENCE 1746 AA; 193767 MW; C0769A3392D6746D CRC64;

Query Match 7.9%; Score 88; DB 10; Length 1746;
Best Local Similarity 21.8%; Pred. No. 15;
Matches 42; Conservative 32; Mismatches 57; Indels 62; Gaps 10;

QY 23 KLKCVSLPKESPSVLLSCCLTVWSFYQVAALQGLA-----SURAELOGHAEK 75
Db 1118 RLKEIINVAKCKTPS-----LTYY-----LRGEAARDAERAKQVQAELOHTTLNHV 1164
QY 76 PAGAKIPEPPAPGEGNSSQNSRNKRAVQGPETVTQDCLQIAD-SETPTTQKGSYTFV 134
Db 1165 TQSTEIYYDP-----NPDVTIADQELVRSYELPDDENSSANLSP 1206
QY 135 WLLSPKFGSALYGVLYTDKTYAMGHLIQRKXVH---VFGD-----ELSLVTLFRCI 183
Db 1207 WLLRLN-----LSKEMTDRKLSMNHV---KNKIHHDGLGDVNVWASENDANLVLIRIA 1259
QY 184 -----QNLDEGE 191
Db 1260 AQKEPEKMAEGEE 1272

RESULT 14
Q55896
ID Q55896 PRELIMINARY; PRT; 240 AA.
AC Q55896;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical protein slr0120.
GN SLR0120.
OS Synechocystis sp. (strain PCC 6803).
```

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
FT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
BT region from map positions 64 to 92% of the genome."
RL DNA Res. 2:153-166 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiura M., Saito S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nariu K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
FT Synechocystis sp. strain PCC6803. II. Sequence determination of the
BT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136 (1996).
DR EMBL; D64004; BAA10658.1; -
DR InterPro; IPR004384; rRNA methyl 1.
DR Pfam; PF00588; SpoU_methylase.
DR ProDom; PD001243; SpoU_methylase; 1.
DR TIGRPFAMs; TIGR00050; rRNA methyl 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 240 AA; 26916 MW; FCIDEA995F5C89A CRC64;

Query Match 7.8%; Score 87.5; DB 16; Length 240;
Best Local Similarity 22.8%; Pred. No. 1.1;
Matches 52; Conservative 27; Mismatches 74; Indels 75; Gaps 10;

QY 1 MDDSTEREQSLTCLKREEMKLECVSILPRKESPSVLLSCCLTVVSVFYQVAALQGD 60
DB 1 MEQGERNVGATARKM---NWGLELILVNR-----C-----DY 33

QY 61 ASLRAELQGHAEKLPAGAKIPEPPAPGEGNSQ---NSRNKRAVQGPETVTQCLQI 117
DB 34 RSEVQATWAVHAKVDLAQAKVDDDLATLGDQRITATSRERILQSPMETPRQ----- 87

QY 118 ADSETPTIQGSYTFVPLLSFKRGSAL-YGQ--VLYTDKTYAMGHLLQKVKVFGDEL 174
DB 88 -----ALPMLLAPNLKLSALVFGREDSGLNEELNQAHRFVRIPVHPQPSL 133

QY 175 SL-----VTLFRCIQ-----NLEEGDELOLAIPRENAQI 203
DB 134 NLSQAVMVCTYELQASLAMETNNQVPGDRLEDGSTMPLA---TNAQL 178

RESULT 15
Q8WON1 PRELIMINARY; PRT; 748 AA.
AC Q8WON1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 82.1 kDa protein.
GN P0681B11.1 OR B1085F01.16.
OS Oryza sativa (Rice), and
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530, 39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC

clone: P0681B11.1";
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
RT clone: B1085F01.1";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003022; BAB78635.1; -
DR EMBL; AP003330; BAB89980.1; -
DR Gramene; Q8WON1; -
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS0109; PROTEIN_KINASE_TYR; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 748 AA; 82079 MW; E18542CC048E36F7 CRC64;

Query Match 7.8%; Score 87.5; DB 10; Length 748;
Best Local Similarity 20.7%; Pred. No. 5.4;
Matches 47; Conservative 39; Mismatches 88; Indels 53; Gaps 10;

QY 16 LKREEMKLEK-CVSIILPRKESPSVL-----LSCCLTVVSVFYQVAALQGD 60
DB 155 LKHEEKHCVEELQCNIVVMKRSQKVVNLNLVGSFKDKSKVCSLPPMLDSSVGKTTTDV 214

QY 61 ASLRAELQGHAEKLPAGAKIPEPPAPGEGNSQNSRNKRAVQGPET 108
DB 215 KEPRTSIRGPAVTPNSPDLETTFTTEAGTSSVSSDPGTSPTSASDTN--GSMKKEAP 272

QY 109 VTQCLQ-----LIADSETPTIQ-KGSYTFVPLLSFKRGSALYQGVLYTDKTYAMGH 163
DB 273 ATKORVGHLDINISDSSETLSPPASFSLQPMVMDILQGSA-----SSRTHGKG---P 322

QY 164 RKKVHVFQDELVLTLFRCIQNLQEGDEL-OLAIIPRENAQISLDGDV 209
DB 323 RRAATATADAL-----LENISKLLDLNLEISSMRSDLNFRGNV 361

Search completed: February 3, 2004, 07:46:50
Job time: 33.0667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 36.3333 Seconds
(without alignments)
952.359 Million cell updates/sec

Title: US-09-911-777-1

Perfect score: 1116

Sequence: 1 MDDSTERQSLTSLCKRE.....ENAIQLSDGVDTFFGALKLL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1042.5	93.4	285	19 AAW73043	Tumour necrosis fa
2	1042.5	93.4	285	19 AAW62461	Human T cell surfa
3	1042.5	93.4	285	19 AAW58391	Homo sapiens neutr
4	1042.5	93.4	285	20 AAY22221	Human TNF α 1 protei
5	1042.5	93.4	285	20 AAY04392	Human Kay-ligand.
6	1042.5	93.4	285	20 AAW93586	Human TNF α 1-alpha
7	1042.5	93.4	285	21 AAB28553	Human TNF α 1. Homo
8	1042.5	93.4	285	21 AAB08659	Amino acid sequenc
9	1042.5	93.4	285	21 AAB08191	

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10 1042.5 93.4 285 21 AAB08261 Amino acid sequenc
11 1042.5 93.4 285 22 AAE09242 Human TALL-1 prote
12 1042.5 93.4 285 22 AAE07156 Human tumour necro
13 1042.5 93.4 285 22 AAE07879 Human BAPF protein
14 1042.5 93.4 285 22 AAU12183 Human PRO738 polyp
15 1042.5 93.4 285 22 AAY71915 Human TAC1-ligand
16 1042.5 93.4 285 22 AAY71978 Human TNF and Apol
17 1042.5 93.4 285 23 AAE28963 Human ZTN4 protein
18 1042.5 93.4 285 23 ABG96458 Human Neutrokine-a
19 1042.5 93.4 285 23 ABG26214 Human neutrokine-a
20 1042.5 93.4 285 23 AAE24636 Human tumour necro
21 1042.5 93.4 285 23 ABB81485 Human ZTNF4 amino
22 1042.5 93.4 285 23 ABJ00715 Human B lymphocyte
23 1042.5 93.4 285 23 ABP47217 Human Blys binding
24 1042.5 93.4 285 23 ABB95471 Human angiogenesis
25 1042.5 93.4 285 23 ABG33576 Human B lymphocyte
26 1042.5 93.4 285 23 ABG33576 Human Neutrokine-a
27 1042.5 93.4 285 23 ABB90325 Human polypeptide
28 1042.5 93.4 285 23 ABB84865 Human PRO738 prote
29 1042.5 93.4 285 23 AAU75409 Neutrokine-alpha (
30 1042.5 93.4 285 23 AAU10942 Human AGP-3. Homo
31 1042.5 93.4 285 24 ABU66581 Human PRO polypept
32 1042.5 93.4 285 24 ABU66857 Human secreted/tra
33 1042.5 93.4 285 24 AAE35212 Human tumour necro
34 1042.5 93.4 285 24 ABP97718 Amino acid sequenc
35 1042.5 93.4 285 24 ABUS9662 Novel secreted and
36 1042.5 93.4 285 24 ABP57103 Membrane bound Bly
37 1042.5 93.4 285 24 ABP60543 Human tumour necro
38 1035.5 92.8 285 21 AAY97037 Membrane bound hum
39 936.5 83.9 264 20 AAW82268 Human NTN-2 protei
40 936.5 83.9 264 20 AAW82270 Human NTN-2 DNA se
41 936.5 83.9 264 21 AAY94005 A human ztnf4, a t
42 927 83.1 266 19 AAW62462 Human T cell surfa
43 927 83.1 266 21 AAB08660 A human neutrokine
44 927 83.1 266 23 ABG96463 Human Neutrokine-a
45 927 83.1 266 23 AAE26215 Human neutrokine-a
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ALIGNMENTS

RESULT 1

AAW73043

ID AAW73043 standard; Protein; 285 AA.

XX AC AAW73043;

XX DT 07-JAN-1999 (first entry)

XX DE Tumour necrosis factor homologue TL5 protein.

XX KW Tumour necrosis factor homologue TL5; vaccine; chronic;
acute inflammation; arthritis; septicemia; autoimmune disease;
inflammatory bowel disease; psoriasis; transplant rejection;
graft vs. host disease; infection; stroke; ischaemia;
acute respirator disease syndrome; testonosis; brain injury; AIDS;
bone disease; cancer; lymphoproliferative disorder; atherosclerosis;
Alzheimer's disease.

XX OS Homo sapiens.

XX PN EP869180-A1.

XX PD 07-OCT-1998.

XX PF 01-APR-1998; 98EP-0302526.

XX PR 03-DEC-1997; 97US-0984396.

XX PR 02-APR-1997; 97US-0041797.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Hurle MR, Young PR;

XX WPI; 1998-508494/44.
 DR N-PSDB; AAV58894.
 XX New tumour necrosis factor homologue, TL5 - useful for diagnosis and
 PT treatment of Alzheimer's disease, AIDS and cancer
 XX
 PS Claim 10; Page 18; 23pp; English.
 XX
 CC The present sequence encodes a tumour necrosis factor homologue TL5
 CC polypeptide sequence. TL5 polypeptides and antibodies are useful for
 CC identifying compounds which agonise and antagonise TL5, and these can be
 CC administered for treatment to inhibit TL5 activity (antagonist) or
 CC enhance TL5 activity (agonist). Gene therapy using the expression system
 CC can also be used to enhance TL5 activity. Diseases or susceptibility to a
 CC disease can be diagnosed by determining the presence or absence of a
 CC mutation in the TL5 protein. TL5 polynucleotides are useful for locating
 CC genes associated with disease by hybridisation to chromosomes. TL5
 CC polypeptides and polynucleotides can be used, especially to raise an
 CC immune response (i.e. as vaccines) for the treatment of chronic and acute
 CC inflammation, arthritis, septicemia, autoimmune diseases (e.g.
 CC inflammatory bowel disease, psoriasis), transplant rejection,
 CC graft vs. host disease, infection, stroke, ischaemia, acute respiratory
 CC disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer
 CC (e.g. lymphoproliferative disorders), atherosclerosis, and Alzheimers
 CC disease.
 XX
 SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 19; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.1e-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
 QY 1 MDDSTERQSLTSLCKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTERQSLTSLCKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
 DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGACAGAPKAGLEAPAVTAGLKIFEPPAP 120
 QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALE 145
 DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALE 180
 QY 146 -----YGOVLYTDKTYANGHLIQKKVHVFGDELSLVTLPFCIQN----- 185
 DB 181 KENKILVKETGYFFIYQGVLYTDKTYANGHLIQKKVHVFGDELSLVTLPFCIQNMPETL 240
 QY 186 -----LEEGDELQLAIPRENAQISLDGDTFFFGALKLL 218
 DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFFGALKLL 285

RESULT 2
 AAW62461
 ID AAW62461 standard; Protein; 285 AA.
 XX AAW62461;
 XX
 DT 05-OCT-1998 (first entry)
 XX
 DE Human T cell surface antigen 63954 protein sequence #2.
 XX
 KW Human; 63954; primate; rodent; mouse; T cell surface antigen; mammal;
 KW diagnosis; antigen-specific proliferation; cytokine production;
 KW immune response; autoimmune disorder; rheumatoid arthritis;
 KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis.
 XX
 OS Homo sapiens.
 XX
 PN W09827114-A2.
 XX

PD 25-JUN-1998.
 XX
 PF 16-DEC-1997; 97WO-US23321.
 XX
 PR 17-DEC-1996; 96US-0033601.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 XX Gorman DM;
 XX
 DR WPI; 1998-362719/31.
 DR N-PSDB; AAV39985.
 XX
 PT New isolated polypeptide, 63954 - used to develop products for
 PT treating e.g. autoimmune disorders, inflammation, tissue rejection,
 PT cancer or degenerative conditions
 XX
 PS Claim 1; Page 60-61; 69pp; English.
 XX

The present sequence is a human T cell surface antigen, designated
 63954. The novel protein designated 63954 is expressed on T cells.
 Protein 63954 can modulate antigen-specific proliferation and cytokine
 production on effector cells and may potentiate immune cell expansion or
 apoptosis. 63954 agonists or antagonists may also act as a co-stimulatory
 molecule for regulation of T cell mediated cell activation, and may cause
 a shift of T helper cell types, e.g. between Th1 and Th2. Antagonists of
 63954 can be used to modulate immune responses in abnormal situations,
 e.g. autoimmune disorders, including rheumatoid arthritis, systemic
 lupus erythematosus (SLE), Hashimoto's autoimmune thyroiditis, as well
 as acute and chronic inflammatory responses in which T cell activation,
 expansion, and/or immunological T cell memory play an important role,
 such as chronic inflammation or tissue rejection. The products can also
 be used in the treatment of conditions associated with abnormal
 physiology or development, including abnormal proliferation, e.g.
 cancerous conditions, or degenerative conditions. The products can also
 be used for detection, diagnosis and drug screening.

SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 19; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.1e-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
 QY 1 MDDSTERQSLTSLCKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTERQSLTSLCKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
 DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGACAGAPKAGLEAPAVTAGLKIFEPPAP 120
 QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALE 145
 DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALE 180
 QY 146 -----YGOVLYTDKTYANGHLIQKKVHVFGDELSLVTLPFCIQN----- 185
 DB 181 KENKILVKETGYFFIYQGVLYTDKTYANGHLIQKKVHVFGDELSLVTLPFCIQNMPETL 240
 QY 186 -----LEEGDELQLAIPRENAQISLDGDTFFFGALKLL 218
 DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFFGALKLL 285

RESULT 3
 AAW58391
 ID AAW58391 standard; Protein; 285 AA.
 XX
 AC AAW58391;
 XX
 DT 11-SEP-1998 (first entry)
 XX
 DE Homo sapiens neutrokin alpha protein.

XX neurokine alpha; cell proliferation; differentiation; migration;
 KW cytotoxicity; cell death; treatment; tumour; infection; inflammation;
 KW wound healing; immunodeficiency; autoimmune disease; graft rejection;
 KW fibrotic disorder; haematopoiesis; sepsis; shock; malaria; HIV; AIDS;
 KW acquired immune deficiency syndrome; rheumatoid arthritis; silicosis;
 XX cachexia; detection; diagnosis; drug screening.

XX Homo sapiens.

OS Key Location/Qualifiers
 FT Domain 1..46
 FT /note= "intracellular domain"
 FT 47..72
 FT /note= "transmembrane domain"
 FT 73..285
 FT /note= "extracellular domain"

XX WO9818921-A1.
 XX 07-MAY-1998.
 XX 25-OCT-1996; 96WO-US17957.
 XX 25-OCT-1996; 96WO-US17957.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ebner R, Ni J, Yu G;
 XX WPI; 1998-272216/24.
 XX N-PSDB; AAV30934.

XX New isolated human Neutrokin alpha - used to develop products for
 PT diagnosis and treatment of e.g. tumours, infections,
 PT immunodeficiencies or autoimmune diseases

XX Claim 17; Fig 1; 104pp; English.

XX The sequence is that of the neutrokin alpha protein.

CC Neutrokin alpha (NA) polypeptides modulate cell proliferation,
 CC differentiation, migration, cytotoxicity and cell death.
 CC They can be used to treat e.g. tumour and tumour metastasis, infections
 CC by bacteria, viruses and other parasites, immunodeficiencies,
 CC inflammatory diseases, lymphadenopathy, autoimmune diseases, graft
 CC versus host disease and to stimulate peripheral tolerance, destroy some
 CC transformed cell lines, mediate cell activation and proliferation, and
 CC are functionally linked as primary mediators of immune regulation and
 CC inflammatory responses. Such activity is useful for immune enhancement
 CC or suppression, myelopoietic control, stem cell mobilisation, acute and
 CC chronic inflammatory control and treatment of leukaemia. They can also
 CC be used to stimulate wound healing and to treat fibrotic disorders
 CC including liver cirrhosis, osteoarthritis and pulmonary fibrosis. They
 CC can also be used to regulate haematopoiesis, by regulating the activation
 CC and differentiation of various haematopoietic progenitor cells, e.g. to
 CC release mature leukocytes from the bone marrow following chemotherapy,
 CC and in stem cell mobilisation. NA may also be used to treat sepsis, NA
 CC antagonists can be used to prevent septic shock, inflammation, cerebral
 CC malaria, activation of the HIV virus, graft-host rejection, bone
 CC resorption, rheumatoid arthritis and cachexia (wasting or malnutrition).
 CC They can also be used to treat e.g. autoimmune diseases such as multiple
 CC sclerosis and insulin-dependent diabetes and inflammatory and infectious
 CC diseases such as silicosis, and sarcoidosis, idiopathic pulmonary
 CC fibrosis, idiopathic hyper-eosinophilic syndrome, endotoxic shock,
 CC atherosclerosis, histamine-mediated allergic reactions and immunological
 CC disorders including late phase allergic reactions, chronic urticaria, and
 CC atopic dermatitis by inhibiting chemokine-induced mast cell and basophil
 CC degranulation and release of histamine. Ige-mediated allergic reactions
 CC such as allergic asthma, rhinitis and eczema, inflammatory pulmonary
 CC diseases, rheumatoid arthritis, inflammation, degenerative and
 CC inflammatory arthropathies, aplastic anaemia, myelodysplastic syndrome,
 CC subepithelial basement membrane fibrosis or adult respiratory distress
 CC syndrome. The products can also be used for detection, diagnosis and

CC drug screening.
 XX Sequence 285 AA;
 SQ
 Query Match 93.4%; Score 1042.5; DB 19; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.1e-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSLCKKREMKLKECVSILPRKESPSV-----LLSCLC 44
 |||||
 DB 1 MDDSTEREQSLTSLCKKREMKLKECVSILPRKESPSVRSKDKGLLAALLALLSCLC 60
 |||||

QY 45 LTVVSFYQVAALQGLDLSRAELQGHAEKLPAGA-----KIPEPPAP 87
 |||||
 DB 61 LTVVSFYQVAALQGLDLSRAELQGHAEKLPAGAPKAGLEBAPAVTAGIKIPEPPAP 120
 |||||

QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIOKGSYTFVPHLLSFKRGSAL-- 145
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 DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIOKGSYTFVPHLLSFKRGSAL-- 180
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QY 146 -----YGVLYTDKTYAMGHILQKVKVHVFQDELSTLTPFCIQN----- 185
 |||||

DB 181 KENKILVKETGYFFIYGVLYTDKTYAMGHILQKVKVHVFQDELSTLTPFCIQNMPETL 240
 |||||

QY 186 -----LSEGEDELQAIIPRENAQISLDGDTFFFGALKLL 218
 |||||

DB 241 PNNSCYSAGIAKLEGEDELQAIIPRENAQISLDGDTFFFGALKLL 285
 |||||

RESULT 4

AAIY22221
 ID AAY22221 standard; Protein; 285 AA.

AC AAY22221;
 XX
 DT 16-SBP-1999 (first entry)
 XX
 DE Human TNFL1 protein sequence.

XX TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
 KW tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
 KW cell differentiation; cytokine production; immunoglobulin; hyperplasia;
 KW apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
 KW myasthenia gravis; insulin-dependent diabetes mellitus; endotoxic shock;
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KW tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
 KW lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
 XX delayed type sensitivity; therapy.

XX Homo sapiens.

OS
 XX
 XX
 PN WO9933980-A2.

XX 08-JUL-1999.

XX 22-DEC-1998; 98WO-US27474.

XX 16-DEC-1998; 98US-0212270.

XX 30-DEC-1997; 97US-0088959.

XX (CHIR) CHIRON CORP.

XX Kassam A, Lamson G, Pot D, Tribouley C;

XX WPI; 1999-405508/34.

XX N-PSDB; AAX84620.

XX New tumour necrosis factor ligands, useful for induction of cell
 XX death and/or proliferation of cells

XX Claim 1; Page 61; 69pp; English.

XX This sequence is the tumour necrosis factor (TNF) ligand family

protein of the invention, designated TNFL1. The TNFL proteins play regulatory roles in cell proliferation and/or differentiation, e.g. they can induce production of cytokines, immunoglobulins, etc. A variety of diseases can be treated by modulating the activity of TNFL proteins, e.g. they can induce apoptosis of activated T cells but rescue resting T cell from apoptosis. TNFL polypeptides can therefore be used to treat autoimmune diseases, such as myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus. TNFL proteins also have tumour stimulating properties, so tumours can be treated by inhibiting the expression or activity of TNFL. Other proliferative disorders, such as neoplasias, dysplasias, and hyperplasia can also be treated using TNFL inhibitors. The TNFL polypeptides and polynucleotides can also be used to enhance or decrease TNF activity, thus providing therapeutic benefit such as induction of cell death, lymphoid organogenesis, or host bacterial resistance, and inhibition of endotoxin shock, contact hypersensitivity, delayed type sensitivity or immunocompetence of a transplant recipient. Tumour necrosis factor (TNF) and its receptors play a major role in host defence and immunosurveillance. As such, there is a need to identify new members of TNFR families. This invention provides this need.

SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 20; Length 285;

Best Local Similarity 76.5%; Pred. No. 1.1e-103;

Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRRSSKDGKLLAATLLALLSCC 60
 QY 45 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
 DB 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
 QY 88 GEGNSSQNRNRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 145
 DB 121 GEGNSSQNRNRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 180
 QY 146 -----YGOVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLRCION----- 185
 DB 181 KENKILVKETGYFFIYGOVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLRCIONMPETL 240
 QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 218
 DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 5

AAV04392

ID AAY04392 standard; Protein; 285 AA.

AC AAY04392;

XX

DT 24-JUN-1999 (first entry)

DE Human Kay-ligand.

DE Kay-ligand; tumour necrosis factor family; TNF; immune system;

KW cytokine; autoimmune disease; tissue graft; cancer; cell death.

XX Homo sapiens.

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PI Tschopp J;

XX

DR WPI; 1999-243715/20.

DR N-PSDB; AAX33330.

XX

PT New human or murine Kay-ligands, members of the tumour necrosis

factor family

XX

PS Claim 12; Page 32; 41pp; English.

XX

CC The present sequence represents human Kay-ligand, which is a member of

the tumour necrosis factor (TNF) family of cytokines. Pharmaceutical

compositions containing the Kay-ligand can be used to suppress or

stimulate the immune system, especially to prevent or reduce the

severity of autoimmune diseases or response to a tissue graft or to

treat cancer. An agent capable of interfering with the Kay-ligand can be

used to induce cell death. The Kay-ligand can also be used to identify

its receptors.

XX

SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 20; Length 285;

Best Local Similarity 76.5%; Pred. No. 1.1e-103;

Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRRSSKDGKLLAATLLALLSCC 60
 QY 45 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
 DB 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
 QY 88 GEGNSSQNRNRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 145
 DB 121 GEGNSSQNRNRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALE 180
 QY 146 -----YGOVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLRCION----- 185
 DB 181 KENKILVKETGYFFIYGOVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLRCIONMPETL 240
 QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 218
 DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 6

AAW93586

ID AAW93586 standard; Protein; 285 AA.

XX

AC AAW93586;

XX

DT 18-JUN-1999 (first entry)

DE Human TNRL1-alpha protein.

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Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4; developmental abnormality; gestational abnormality; prostate cancer; APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; cytoplasmic domain; immunogen; antibody preparation; breast carcinoma; apoptosis; human; TNRL1-alpha.

OS Homo sapiens.

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(UNIW) UNIV WASHINGTON.

XX Chaudhary PM;
 XX WPI; 1999-205191/17.
 DR N-PSDB; AAX23420.
 XX New Tumor Necrosis Factor family receptor polypeptides and ligands -
 PT useful for diagnosis and treatment of prostate cancer and
 PT developmental or gestational abnormalities
 XX
 PS Claim 34; Fig 11A; 156pp; English.
 XX
 CC This invention describes isolated Tumor Necrosis Factor (TNF) family
 CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
 CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 CC their active fragments. APO4 is useful for diagnosing prostate cancer
 CC by determining levels of APO4 in an individual. Prostate cancer can also
 CC be treated using APO4 selective binding agents linked to a therapeutic
 CC moiety. APO4 polypeptides are also useful for identifying selective
 CC binding agents, useful in diagnosis/treatment of disease by binding of
 CC agents to the polypeptide/active fragment which is extracellular, or
 CC expressed on the cell surface. The binding is preferably performed in
 CC vivo. APO4 polypeptides/active fragments are also useful for screening
 CC for agonists and antagonists by binding and observing the change in APO4
 CC activity. Effective pharmacological agents useful in diagnosis or
 CC treatment of disease are also identified using APO4 polypeptides/active
 CC fragments and APO4 signal transducer molecules that specifically interact
 CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 CC activity. The method is performed in vivo or in vitro. APO polypeptides
 CC are all useful as immunogens for preparing antibodies. APO4 is also
 CC useful for diagnosis/treatment of developmental or gestational
 CC abnormalities. APO8 was transfected to human breast carcinoma cell line
 CC MCF-7, and induced apoptosis.
 XX
 SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 20; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.1e-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
 DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGIKIFEPAP 120
 QY 88 GEGNSSQNSNRKRAVOGPEETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSAL-- 145
 DB 121 GEGNSSQNSNRKRAVOGPEETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSAL-- 180
 QY 146 -----YGVLYTDKTYAMGHLIQRKVVHVFGEDELSTLTLFRCIQN----- 185
 DB 181 KENKILVKETGYFFTYGVLYTDKTYAMGHLIQRKVVHVFGEDELSTLTLFRCIQNMPETL 240
 QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 218
 DB 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 7
 ID AAB28553
 XX AAB28553 standard; protein; 285 AA.
 AC AAB28553;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human TNFL1.
 XX
 KW Human; tumour necrosis factor like-1; TNFL1; tumour necrosis factor; TNF;
 KW immunosuppressive; antiarthritic; neuroprotective; dermatological;

KW antiinflammatory; antidiabetic; cytostatic; osteopathic; gene therapy;
 KW colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;
 KW osteoporosis; autoimmune disease; myasthenia gravis;
 KW insulin-dependent diabetes mellitus.
 XX Homo sapiens.
 OS WO2000060079-A2.
 PN 12-OCT-2000.
 XX
 PD 05-APR-2000; 2000WO-US09058.
 PF 05-APR-1999; 99US-0286529.
 PR (CHIR) CHIRON CORP.
 PA Tribouley C;
 PI WPI; 2000-665004/64.
 XX N-PSDB; AAC63756.
 PT Tumor necrosis factor (TNF) and TNF receptor superfamily protein
 PT members TNF-L and TNFR-L, useful for enhancing or decreasing TNF
 PT activities such as inducing cell death and lymphoid organogenesis
 PS Claim 1; Page 65; 77pp; English.
 XX
 CC The present sequence is given in a specification relating to an isolated
 CC human protein designated tumour necrosis factor like-1 (TNFL1). It may be
 CC used to induce cell death in tumours, to induce apoptosis of activated T
 CC cells, to induce inflammation, and to rescue resting T cells from
 CC apoptosis. TNF receptors are used to regulate the function of a TNF
 CC ligand which plays a role in apoptosis, inflammation, differentiation, or
 CC proliferation. Expression of the receptors can also be useful as markers
 CC for cancer, especially for colon cancer. Diseases which can be treated
 CC using ligands and/or receptors of the TNF/TNFR superfamily include
 CC rheumatoid arthritis, cancer, septic shock, Crohn's disease and
 CC osteoporosis. The polynucleotides can be used in gene delivery vehicles,
 CC for the purpose of delivering a mRNA or oligonucleotide, full-length
 CC protein, fusion protein, polypeptide, or ribozyme, or single-chain
 CC antibody, into a cell. The newly identified receptor proteins play
 CC regulatory roles in cell proliferation and/or differentiation. The
 CC receptors can also play a role in the negative regulation of
 CC osteoclastogenesis. Soluble TNFR-like receptors can be useful in the
 CC neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be
 CC used to treat autoimmune diseases (myasthenia gravis and
 CC insulin-dependent diabetes mellitus), tumours, and proliferative
 CC disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be
 CC delivered to subjects for the purpose of screening test compounds for
 CC those which are useful for enhancing transfer of TNF-L subgenomic
 CC polynucleotides to the cell or for enhancing subsequent biological
 CC effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.

Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 21; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.1e-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
 DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
 DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGIKIFEPAP 120
 QY 88 GEGNSSQNSNRKRAVOGPEETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSAL-- 145
 DB 121 GEGNSSQNSNRKRAVOGPEETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSAL-- 180
 QY 146 -----YGVLYTDKTYAMGHLIQRKVVHVFGEDELSTLTLFRCIQN----- 185

Db 181 KENKILVKETGYFFTYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLTFRCIQNMPETL 240
Qy 186 -----LEEGDELQAIIPRENAQISLDGVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQAIIPRENAQISLDGVTFFGALKLL 285

RESULT 8

AAB08659
ID AAB08659 standard; Protein; 285 AA.

AC AAB08659;

DT 02-JAN-2001 (first entry)

XX Amino acid sequence of a human neutrokin-alpha polypeptide.

XX Human; neutrokin-alpha; tumor; tumor metastasis; infection;
KW immunodeficiency; inflammatory disease; lymphadenopathy; dermatitis;
KW autoimmune disease; graft versus host disease; immune regulation;
KW severe combined immunodeficiency-X-linked agammaglobulinemia;
KW kappa chain deficiency; B cell lymphoproliferative disorder; purpura;
KW Wiskott-Aldrich syndrome; systemic lupus erythematosus; myocarditis;
KW idiopathic thrombocytopenia purpura; hemolytic anemia; neuritis;
KW allergic encephalomyelitis; relapsing polychondritis; glomerulonephritis;
KW rheumatic heart disease; multiple sclerosis; uveitis; ophthalmia;
KW polyendocrinopathy; Reiter's disease; autoimmune pulmonary inflammation;
KW myeloprotection; stem cell mobilization; leukemia.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..46 /note= "intracellular domain"

FT Domain 47..72 /note= "transmembrane domain"

FT Domain 73..285 /note= "extracellular domain"

FT Modified-site 124..127 /note= "potential N-linked glycosylation site"

FT Modified-site 242..245 /note= "potential N-linked glycosylation site"

FT /note= "potential N-linked glycosylation site"

XX WO200050597-A2.

PN 31-AUG-2000.

PD 22-FEB-2000; 2000WO-US04336.

PF 23-FEB-1999; 99US-0255794.

PR 02-MAR-1999; 99US-0122388.

PR 12-MAR-1999; 99US-0124097.

PR 26-MAR-1999; 99US-0126599.

PR 02-APR-1999; 99US-0127598.

PR 16-APR-1999; 99US-0130412.

PR 23-APR-1999; 99US-0130696.

PR 27-APR-1999; 99US-0131278.

PR 29-APR-1999; 99US-0131673.

PR 28-MAY-1999; 99US-0136784.

PR 06-JUL-1999; 99US-0142659.

PR 27-JUL-1999; 99US-0145824.

PR 24-NOV-1999; 99US-0167239.

PR 03-DEC-1999; 99US-0168624.

PR 16-DEC-1999; 99US-0171108.

PR 23-DEC-1999; 99US-0171626.

PR 14-JAN-2000; 2000US-0176015.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Ni J, Ebner R, Yu G;

PI WPI; 2000-572093/53.

XX

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DR N-ESDB; AAA64427.
XX Novel cytokine neutrokin-alpha, its splicing variant, neutrokin-alpha
PT SV polypeptides useful for treating tumor, tumor metastasis, microbial
FT infections, immunodeficiency, inflammatory diseases, lymphadenopathy
PS
XX Claim 18; Fig 1A-B; 414pp; English.

XX The present sequence represents a human neutrokin-alpha polypeptide.
CC Neutrokin-alpha polypeptides are used to treat, prevent, prognosis and
CC diagnose tumor and tumor metastasis, infections by bacteria, viruses
CC and other parasites, immunodeficiencies, inflammatory diseases,
CC lymphadenopathy, autoimmune diseases, graft versus host disease, to
CC mediate immune regulation and inflammatory responses. Diseases which
CC may be treated include severe combined immunodeficiency (SCID)-X-linked
CC agammaglobulinemia, kappa chain deficiency, B cell lymphoproliferative
CC disorder (BLPD), Wiskott-Aldrich syndrome, systemic lupus erythematosus,
CC idiopathic thrombocytopenia purpura, hemolytic anemia, dermatitis,
CC allergic encephalomyelitis, myocarditis, relapsing polychondritis,
CC rheumatic heart disease, glomerulonephritis, multiple sclerosis,
CC Neuritis, Uveitis Ophthalmia, Polyendocrinopathies, Purpura
CC (e.g. Henrich-Scoenlein purpura), Reiter's Disease, and Autoimmune
CC Pulmonary Inflammation. Neutrokin-alpha is useful for immune
CC enhancement or suppression, myeloprotection, stem cell mobilization,
CC acute and chronic inflammatory control and treatment of leukemia.

XX Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 21; Length 285;
Best Local Similarity 76.5%; Pred. No. 1.1e-103;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

Qy 1 MDDSTEREQSLTSCLEKREMKLKECVSILPRKESPSV-----LLSCC 44

Db 1 MDDSTEREQSLTSCLEKREMKLKECVSILPRKESPSVSSKDKGLAATLLALLSCC 60

Qy 45 LTVVSFYQVAALQDGLASRAELQGHAEKLPAGA-----KIFEPPAP 87

Db 61 LTVVSFYQVAALQDGLASRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120

Qy 88 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSTPTIQGSYTFVPWLLSFKGSAL-- 145

Db 121 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSTPTIQGSYTFVPWLLSFKGSAL 180

Qy 146 -----YGOVLYTDKTYAMGHLIQKRVHVFGEDELSTLTFRCIQN----- 185

Db 181 KENKILVKETGYFFTYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLTFRCIQNMPETL 240

Qy 186 -----LEEGDELQAIIPRENAQISLDGVTFFGALKLL 218

Db 241 PNNCSYAGIAKLEEGDELQAIIPRENAQISLDGVTFFGALKLL 285

RESULT 9

AAB08191

ID AAB08191 standard; Protein; 285 AA.

XX AAB08191;

AC AAB08191;

DT 04-DEC-2000 (first entry)

XX Amino acid sequence of human cytokine designated THANK.

DE Human; cytokine; THANK; tumour necrosis factor homologue; apoptosis;

XX nuclear factor-KB; c-jun N-terminal kinase; shock; acute phase response;

KW viral infection; radiation susceptibility; atherosclerosis; cancer;

KW acute inflammatory condition; arthritis; allergy;

KW graft versus host reaction; tumour cell.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

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FT Domain 1..46
FT /note= "intracellular domain"
FT FT 47..77
FT /note= "transmembrane domain"
FT FT 78..111
FT /note= "extracellular domain"
FT FT 112..285
FT /note= "extracellular domain"
XX WO200045836-A1.
XX
XX PD 10-AUG-2000.
XX
XX PF 02-FEB-2000; 2000WO-US02751.
XX
XX PR 02-FEB-1999; 99US-0118531.
XX
XX PA (RERE-) RES DEV FOUND.
XX
XX PI Aggarwal BB;
XX
XX PN WPI; 2000-514890/46.
XX
XX PD Inhibiting the activation of nuclear factor-kB in cells for treating
XX PT pathological conditions comprises treating cells with a tumour necrosis
XX PT factor homolog inhibitor -
XX
XX PS Example 1; Fig 1; 45pp; English.
XX
XX CC The present sequence represents a human cytokine, designated THANK.
XX CC THANK is a tumour necrosis factor (TNF) homologue that activates
XX CC apoptosis, nuclear factor-kB, and c-Jun N-terminal kinase. Inhibitors of
XX CC the THANK polypeptide are used to inhibit the activation of nuclear
XX CC factor-kB in cells. The method is used to inhibit the activation of
XX CC nuclear factor-kB in cells, treat pathological conditions such as toxic
XX CC and septic shock, acute phase response, viral infection, radiation
XX CC susceptibility, atherosclerosis, cancer, acute inflammatory conditions,
XX CC arthritis, allergy, and graft versus host reaction, and inhibit growth
XX CC of tumour cells such as myeloid cells, colon cancer cells, prostate
XX CC cancer cells, cervical carcinoma cells, chronic myeloid leukemic cells
XX CC and acute myeloid leukemic cells.
XX
XX SQ Sequence 285 AA;
XX
XX Query Match 93.4%; Score 1042.5; DB 21; Length 285;
XX Best Local Similarity 76.5%; Pred. No. 1.1e-103;
XX Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
XX
QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDKGLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGLDASLRRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGLDASLRRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSIYTFVFWLLSFKRGSAL-- 145
Db 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSIYTFVFWLLSFKRGSAL 180
QY 146 -----YGVLYTDKTYAMGHLIQRKKVHVFGDELSTLFRCIQN----- 185
Db 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKKVHVFGDELSTLFRCIQNMPETL 240
QY 186 -----LESGDELOLAIPRENAQISLDGVTFFGALKLL 218
Db 241 PNNCSYAGIAKLESGDELOLAIPRENAQISLDGVTFFGALKLL 285
XX
XX RESULT 10
XX AAB08261
XX ID AAB08261 standard; Protein; 285 AA.
XX

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AC AAB08261;
XX
XX DT 04-DEC-2000 (first entry)
XX
XX DE Amino acid sequence of a human AGP-3 polypeptide.
XX
XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
XX KW type II transmembrane protein; B cell stimulatory factor;
XX KW inflammatory disorder; immune disorder; rheumatoid arthritis;
XX KW lupus and graft versus host disease.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Domain 1..46
XX FT /note= "intracellular domain"
XX FT Region 42..72
XX FT /note= "transmembrane region"
XX FT Domain 73..285
XX FT /note= "extracellular domain"
XX
XX PN WO200047740-A2.
XX
XX PD 17-AUG-2000.
XX
XX PF 11-FEB-2000; 2000WO-US03653.
XX
XX PR 12-FEB-1999; 99US-0119906.
XX PR 18-NOV-1999; 99US-0166271.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX PI Boyle WJ, Hsu H;
XX
XX DR WPI; 2000-558217/51.
XX DR N-PSDB; AAA63941.
XX
XX PT Novel polypeptides comprising tumour necrosis factor ligand family
XX PT proteins, useful for treating inflammatory and immune disorders, e.g.
XX PT rheumatoid arthritis -
XX
XX PS Claim 4; Fig 1; 71pp; English.
XX
XX CC The present sequence represents a human AGP-3 polypeptide. AGP-3 is a
XX CC tumour necrosis factor (TNF) ligand family member. AGP-3 is a type II
XX CC transmembrane protein, and is a potent B cell stimulatory factor.
XX CC Expression of AGP-3 correlates to increases in the number of B cells
XX CC and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic
XX CC acids may be used to treat inflammatory and immune disorders,
XX CC e.g. rheumatoid arthritis, Crohn's disease, lupus and graft versus
XX CC host disease. The nucleic acids may be used to regulate the expression
XX CC of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic
XX CC acids are also useful for the detection of AGP-3 agonists, antagonists
XX CC and characterizing interactions with AGP-3 related proteins.
XX CC note: this sequence is not specifically claimed. It is only mentioned
XX CC in the claims, in that a polypeptide that does not comprise the present
XX CC sequence is claimed.
XX
XX SQ Sequence 285 AA;
XX
XX Query Match 93.4%; Score 1042.5; DB 21; Length 285;
XX Best Local Similarity 76.5%; Pred. No. 1.1e-103;
XX Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
XX
QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDKGLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGLDASLRRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGLDASLRRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSIYTFVFWLLSFKRGSAL-- 145

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Db 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPPWLLSFKRGSALEE 180
Qy 146 -----YGOVLYTDKTYANGHLIQRKKVHVFGDELSTVTLFRCION----- 185
Db 181 KENKILVKETGYFFIYGOVLYTDKTYANGHLIQRKKVHVFGDELSTVTLFRCIONMPETL 240
Qy 186 -----LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285

RESULT 11
AAE09242
ID AAE09242 standard; Protein; 285 AA.
AC AAE09242;
XX
DT 19-NOV-2001 (first entry)
DE Human TALL-1 protein.
KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX
OS Homo sapiens.
XX
PN WO2000160397-A1.
XX
PD 23-AUG-2001.
XX
PF 28-NOV-2000; 2000WO-US32378.
XX
PR 16-FEB-2000; 2000US-0182938.
PR 22-AUG-2000; 2000US-0226986.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
PI Yan W;
XX
DR WPI; 2001-541628/60.
DR N-PSDB; AAD15903.
XX
PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists -
XX
PS Claim 2; Fig 3; 160pp; English.
XX
CC The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
CC e.g. TACI or BCMA. The method is useful for treating pathological
CC conditions or diseases associated with increased TALL-1 and APRIL
CC expression or activity. TALL-1 and APRIL antagonists are used to
CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
CC They are useful for treating a mammal suffering from cancer such
CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
CC psoriasis and lupus erythematosus. The present sequence is human
CC TALL-1 protein.
XX
SQ Sequence 285 AA;
Query Match 93.4%; Score 1042.5; DB 22; Length 285;
Best Local Similarity 76.5%; Pred. No. 1.1e-103;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
Qy 1 MDDSTEREQSLTSCLEKREEMKLEKCVSLPRKESPSVRSSKDGKLLAATLLALLSSCC 44

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Db 1 MDDSTEREQSLTSCLEKREEMKLEKCVSLPRKESPSVRSSKDGKLLAATLLALLSSCC 60
Qy 45 LTVVSFYQVAALQGDLASRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGDLASRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
Qy 88 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPPWLLSFKRGSALE-- 145
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Qy 146 -----YGOVLYTDKTYANGHLIQRKKVHVFGDELSTVTLFRCION----- 185
Db 181 KENKILVKETGYFFIYGOVLYTDKTYANGHLIQRKKVHVFGDELSTVTLFRCIONMPETL 240
Qy 186 -----LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285

RESULT 12
AAE07156
ID AAE07156 standard; Protein; 285 AA.
AC AAE07156;
XX
DT 06-NOV-2001 (first entry)
DE Human tumour necrosis factor (TNF)-delta protein.
KW Human; tumour necrosis factor; TNF-delta; gene therapy; antirheumatic;
KW apoptosis; rheumatoid arthritis; cytostatic; sepsis; anti-inflammatory;
KW inflammatory bowel disease; immunosuppressive; antiarthritic; tumour;
KW antibacterial; cancer.
XX
OS Homo sapiens.
XX
PN US2001010925-A1.
XX
PD 02-AUG-2001.
XX
PF 17-NOV-1997; 97US-0971317.
XX
PR 17-NOV-1997; 97US-0971317.
XX
PA (WILEY) WILEY S R.
XX
PI Wiley SR;
XX
DR WPI; 2001-496166/54.
DR N-PSDB; AAD13435.
XX
PT New tumor necrosis factors (TNF)-delta polynucleotide and polypeptide,
PT useful in gene therapy, particularly for treating inflammation, and for
PT inducing apoptosis in cancer and tumor-associated cells to treat cancer
-
XX
PS Claim 16; Page 36-37; 46pp; English.
XX
CC The present sequence is human tumor necrosis factor (TNF)-delta protein.
CC The TNF-delta polynucleotide is useful in gene therapy for modulating
CC TNF-delta. TNF-delta is useful for treating deficiencies of TNF-delta
CC and diseases ameliorated by TNF-delta. TNF-delta is also useful for
CC screening, diagnosing, prognosing, staging or monitoring conditions
CC or diseases attributable to TNF-delta, e.g. inflammation (e.g.
CC inflammatory bowel disease, sepsis or rheumatoid arthritis). The
CC TNF-delta is also useful as an anti-cancer agent to induce apoptosis in
CC cancer and tumour-associated cells.
XX
SQ Sequence 285 AA;
Query Match 93.4%; Score 1042.5; DB 22; Length 285;
Best Local Similarity 76.5%; Pred. No. 1.1e-103;

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Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCLEEMKKECVSILPRKESPSV-----LLSCC 44
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 QY 45 LTVVSFYQVAALQGDLSRAELQGHAEKLPAGA-----KIFEPAP 87
 Db 61 LTVVSFYQVAALQGDLSRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
 QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVWLLSFKGSAL-- 145
 Db 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVWLLSFKGSAL-- 180
 QY 146 -----YGVLYTDTKYAMGHLIQKRVHVFGEDELSTVLFRCIQN----- 185
 Db 181 KENKILVKETGYFFIYQVLYTDTKYAMGHLIQKRVHVFGEDELSTVLFRCIQNMPETL 240
 QY 186 -----LEGEDELQAIAPRENAQISLDGVDVTFFGALKLL 218
 Db 241 PNNSCYSAGIAKLEEGDELQAIAPRENAQISLDGVDVTFFGALKLL 285

RESULT 13

AAE07879 ID AAE07879 standard; Protein; 285 AA.

AAE07879; AC

DT 01-NOV-2001 (first entry)

DE Human BAFF protein.

KW Human; tumour necrosis factor; TNF; APRIL; BAFF; therapy; melanoma;
 KW immune system-related disorder; cancer; renal cell; breast; stomach;
 KW rectal; colon; throat; bladder; ovarian carcinoma; cellular disorder;
 KW gastrointestinal; scleroderma; Kaposi's sarcoma; chronic leukaemia;
 KW squamous cell carcinoma; hyperproliferative condition; pannus formation;
 KW rheumatoid arthritis; postsurgical scarring; fibrosis; liver; uterine;
 KW lung; immunodeficiency; inflammatory disease; lymphadenopathy; vulnary;
 KW autoimmune disease; graft versus host disease; dermatological;
 KW antiinflammatory; immunosuppressive; cytostatic.

OS Homo sapiens.

Key Location/Qualifiers
 Domain 1..46
 /label= Intracellular_domain
 Domain 47..72
 /label= Transmembrane_domain
 Domain 73..285
 /label= Extracellular_domain

XX WO200158949-A2.

XX 16-AUG-2001.

XX 08-FEB-2001; 2001WO-US04121.

XX 11-FEB-2000; 2000US-0181670.

XX (BIOJ) BIOGEN INC.

XX Rennett PD, Thompson JS, Ambrose C, Cachero TG;

XX WPI; 2001-514644/56.

XX N-PSDB; AAD14417.

XX New heteromeric ligand of tumor necrosis factor (TNF) family, useful
 PT for diagnosis, treatment of immune system-related disorders in humans,
 PT comprises TNF-family member APRIL subunit linked non-covalently to
 PT TNF-family member BAFF subunit

PS Claim 2; Fig 2b; 42pp; English.

XX The present invention relates to an isolated heteromeric ligand of
 CC tumour necrosis factor (TNF)-family, referred to as APBF comprising a
 CC TNF-family member APRIL subunit linked non-covalently to TNF-family
 CC member BAFF subunit. APBF is useful for diagnosis or treatment of
 CC various immune system-related disorders in mammals, preferably humans.
 CC Such disorders include cancer, including cellular disorders, for e.g.
 CC renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer,
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma,
 CC colon cancer, bladder cancer, squamous cell carcinoma and
 CC gastrointestinal or stomach cancer, cellular hyperproliferative
 CC conditions, such as scleroderma, pannus formation in rheumatoid
 CC arthritis, postsurgical scarring and lung, liver and uterine fibrosis
 CC and immunodeficiencies, inflammatory diseases, lymphadenopathy,
 CC autoimmune diseases and graft versus host disease. APBF is also useful
 CC for producing monoclonal or polyclonal antibodies and for identifying
 CC novel modulators affecting biological function and receptors interacting
 CC with APBF. The present sequence is human BAFF protein.

XX Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 22; Length 285;

Best Local Similarity 76.5%; Pred. No. 1.1e-103;

Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCLEEMKKECVSILPRKESPSV-----LLSCC 44

Db 1 MDDSTEREQSLTSCLEEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60

QY 45 LTVVSFYQVAALQGDLSRAELQGHAEKLPAGA-----KIFEPAP 87

Db 61 LTVVSFYQVAALQGDLSRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120

QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVWLLSFKGSAL-- 145

Db 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVWLLSFKGSAL-- 180

QY 146 -----YGVLYTDTKYAMGHLIQKRVHVFGEDELSTVLFRCIQN----- 185

Db 181 KENKILVKETGYFFIYQVLYTDTKYAMGHLIQKRVHVFGEDELSTVLFRCIQNMPETL 240

QY 186 -----LEGEDELQAIAPRENAQISLDGVDVTFFGALKLL 218

Db 241 PNNSCYSAGIAKLEEGDELQAIAPRENAQISLDGVDVTFFGALKLL 285

RESULT 14

AAU12183 ID AAU12183 standard; Protein; 285 AA.

XX AAU12183;

XX 24-OCT-2001 (first entry)

XX Human PRO738 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX WO200140466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US32678.

XX 01-DEC-1999; 99WO-US28301.

XX 01-DEC-1999; 99WO-US28634.

XX 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;
 XX
 DR WPI; 2001-408281/43.
 DR N-PSDB; AAS21255.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 PS Claim 12; Fig 24; 813pp; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PMNCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 SQ Sequence 285 AA;
 Query Match 93.4%; Score 1042.5; DB 22; Length 285;
 Best Local Similarity 76.5%; Pred. No. 1.le-103;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
 QY 1 MDDSTERQSRITSLCKREEMKKECVSILPKRESPSV-----LLSCC 44
 DB 1 MDDSTERQSRITSLCKREEMKKECVSILPKRESPSVRSSKGGKLLAATILLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPAP 87

Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAEPAPAVTAGLKIFEPAP 120
 QY 88 GEGNSSNSNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVFWLLSFKRGSAL-- 145
 Db 121 GEGNSSNSNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVFWLLSFKRGSAL 180
 QY 146 -----YQGVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCION----- 185
 Db 181 KENKILVKETGYPIYGVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLPFCIONMPETL 240
 QY 186 -----LEEGDELOLAIPRENAQISLDGDTFFGALKLL 218
 Db 241 PNNSCYSAGIAKLEEGDELOLAIPRENAQISLDGDTFFGALKLL 285
 RESULT 15
 AAY71915
 ID AAY71915 standard; Protein; 285 AA.
 XX
 XX AC AAY71915;
 XX AC
 DT 26-MAR-2001 (first entry)
 XX
 DE Human TACI-ligand (TACI-L) protein.
 XX
 KW Human; transmembrane activator and CAML interactor; TACI;
 KW tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;
 KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;
 KW neutrokinine alpha polypeptide; TACI-ligand; TACI-L; cytostatic; therapy;
 KW neuroprotective; antidiabetic; antiviral; antinflammatory; tumour;
 KW antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis;
 KW rheumatoid arthritis; graft rejection; inflammation; cell proliferation;
 KW cell death; immunoglobulin E-mediated allergic reaction; Ige.
 XX
 OS Homo sapiens.
 XX
 FH Domain
 FT 1..46
 FT /label= Intracellular_domain
 FT Domain
 FT 47..72
 FT /label= Transmembrane_domain
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 FT 73..285
 FT /label= Extracellular_domain
 FT Binding-site
 FT 123..285
 FT /label= TACI binding site
 FT /note= "Binds with extracellular domain of TACI"
 XX
 WO200067034-A1.
 XX
 PD 09-NOV-2000.
 XX
 PD 14-APR-2000; 2000WO-US10282.
 XX
 PR 30-APR-1999; 99US-0302863.
 XX
 PA (IMMU) IMMUNEX CORP.
 XX
 PI Goodwin RG, Din WS;
 XX
 DR WPI; 2001-016005/02.
 DR N-PSDB; AAD02007.
 XX
 PT Use of new interactions between tumour necrosis factor receptors (TACI)
 PT and TACI ligands to screen candidate molecules for determining agonist
 PT and antagonist interactions which are used for treating inflammation -
 XX
 PS Claim 10; Fig 2b; 46pp; English.
 XX
 CC The present sequence is a human tumour necrosis factor receptor
 CC (TACI)-ligand (TACI-L) protein.
 CC TACI (Transmembrane activator and calcium-signal modulating
 CC cyclophilin ligand (CAML)-interactor) forms a complex with neutrokin

CC alpha polypeptide (TACI-Ligand). The antagonist or agonist of
CC TACI/TACI-L complex is useful for modulating an intracellular signalling
CC cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L
CC complex are used to inhibit the interaction between TACI and TACI-L for
CC therapeutic purposes to treat tumour and tumour metastasis and to combat
CC various autoimmune diseases e.g. multiple sclerosis and diabetes, as
CC well as other disorders, such as viral infection, rheumatoid arthritis,
CC graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions
CC and inflammation. The interaction is used to study cellular processes
CC associated with tumour necrosis factor (TNF)-receptors such as immune
CC regulation, cell proliferation, cell death and inflammatory responses.
CC The interaction between the extracellular region of TACI and TACI-L can
CC be used to further develop understanding of which cell types TACI-L
CC acts upon.
XX
SQ Sequence 285 AA;

Query Match 93.4%; Score 1042.5; DB 22; Length 285;

Best Local Similarity 76.5%; Pred. No. 1.1e-103;

Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCLEKREMKKECVSILPRKESPSV-----LLSCC 44

DB 1 MDDSTEREQSLTSCLEKREMKKECVSILPRKESPSVSRSSKOGKLLAATLLALLSCC 60

QY 45 LTVVSFYQVAALQGLASLRAELQGHAEKLPAGA-----KIPEPPAP 87

DB 61 LTVVSFYQVAALQGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120

QY 88 GEGNSSQNSRNKRAVQGPETVTQCLQIADSETPTIQKGYTFVPWLLSPKRGSALE 145

DB 121 GEGNSSQNSRNKRAVQGPETVTQCLQIADSETPTIQKGYTFVPWLLSPKRGSALEE 180

QY 146 -----YGOVLYTDKTYAMGHILQKRVHVGDELSTVLFRCION----- 185

DB 181 KENKILVKETGYFFYIGQVLYTDKTYAMGHILQKRVHVGDELSTVLFRCIONMPETL 240

QY 186 -----LEEGDELQLAIPRENAQISLDGDVTFPGALKLL 218

DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDVTFPGALKLL 285

Search completed: February 3, 2004, 07:48:16

Job time : 38.3333 secs

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2	1116	100.0	218	15	US-10-045-574A-1	Sequence 1, Appli
3	1042.5	93.4	285	8	US-08-971-317A-2	Sequence 2, Appli
4	1042.5	93.4	285	9	US-09-193-663-2	Sequence 2, Appli
5	1042.5	93.4	285	9	US-09-877-156-1	Sequence 1, Appli
6	1042.5	93.4	285	9	US-09-879-919-23	Sequence 2, Appli
7	1042.5	93.4	285	10	US-09-929-493-2	Sequence 2, Appli
8	1042.5	93.4	285	10	US-09-779-050A-2	Sequence 2, Appli
9	1042.5	93.4	285	11	US-09-302-863-4	Sequence 4, Appli
10	1042.5	93.4	285	11	US-09-880-748-3228	Sequence 3228, Appli
11	1042.5	93.4	285	11	US-09-932-613-173	Sequence 173, Appli
12	1042.5	93.4	285	12	US-10-137-870-24	Sequence 24, Appli
13	1042.5	93.4	285	12	US-10-140-018-24	Sequence 24, Appli
14	1042.5	93.4	285	12	US-10-140-021-24	Sequence 24, Appli
15	1042.5	93.4	285	12	US-10-140-274-24	Sequence 24, Appli

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; Sequence 1, Application US/10045574A
; Publication NO. US20030095967A1
; GENERAL INFORMATION:
; APPLICANT: MACKAY, Fabienne
; APPLICANT: KALLIED, Susan
; TITLE OF INVENTION: BARR, Inhibitors Thereof and Their Use
; TITLE OF INVENTION: in the Modulation of B-Cell Response and Treatment of
; TITLE OF INVENTION: Autoimmune Disorders
; FILE REFERENCE: 08201.0024-01000
; CURRENT APPLICATION NUMBER: US/10/045,574A
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/911,777
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-045-574A-1

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RESULT, T 3

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RESULTS 3
US-08-971-317A-2
; Sequence 2, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,317A
FILING DATE: 17-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Goller, Mimi C
REGISTRATION NUMBER: 39,046
REFERENCE/DOCKET NUMBER: 6255.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
TELEFAX: (847) 938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-2

RESULT. T 4

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RES001 4
US-09-193-663-2
; Sequence 2, Application US/09193663
; Patent No. US2002005624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255 US.02
; CURRENT APPLICATION NUMBER: US/09/193,663
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17

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; CURRENT FILING DATE: 2001-08-15
 ; PRIOR APPLICATION NUMBER: 60/225,628
 ; PRIOR FILING DATE: 2000-08-15
 ; PRIOR APPLICATION NUMBER: 60/227,008
 ; PRIOR FILING DATE: 2000-08-23
 ; PRIOR APPLICATION NUMBER: 60/234,338
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: 60/240,806
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/250,020
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-06
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/296,122
 ; PRIOR FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: 60/304,809
 ; PRIOR FILING DATE: 2001-07-13
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 285
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-929-493-2

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 Best Local Similarity 76.5%; Pred. No. 7.7e-106;
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 QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
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 Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
 QY 88 GEGNSSONRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALE 145
 Db 121 GEGNSSONRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALE 180
 QY 146 -----YQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQN----- 185
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 QY 186 -----LEEGDELQALIPRENAQISLDGDTFFFGALKLL 218
 Db 241 PNNCYSAGIAKLEEGDELQALIPRENAQISLDGDTFFFGALKLL 285

RESULT 8
 US-09-779-050A-2
 ; Sequence 2, Application US/09779050A
 ; Patent No. US20020160416A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOYLE, WILLIAM
 ; APPLICANT: HSU, WILLIAM
 ; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
 ; FILE REFERENCE: A-570B
 ; CURRENT APPLICATION NUMBER: US/09/779,050A
 ; CURRENT FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: 60/181,800
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: Patent In version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 285
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-779-050A-2

Query Match 93.4%; Score 1042.5; DB 10; Length 285;
 Best Local Similarity 76.5%; Pred. No. 7.7e-106;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
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 Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
 Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
 QY 88 GEGNSSONRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALE 145
 Db 121 GEGNSSONRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALE 180
 QY 146 -----YQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQN----- 185
 Db 181 KENKILVKETGYFFIYQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQNMPETL 240
 QY 186 -----LEEGDELQALIPRENAQISLDGDTFFFGALKLL 218
 Db 241 PNNCYSAGIAKLEEGDELQALIPRENAQISLDGDTFFFGALKLL 285

RESULT 9
 US-09-302-863-4
 ; Sequence 4, Application US/09302863
 ; Publication No. US2003002233A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodwin, Raymond G
 ; APPLICANT: Din, Wanwan S
 ; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
 ; FILE REFERENCE: 2519
 ; CURRENT APPLICATION NUMBER: US/09/302,863
 ; CURRENT FILING DATE: 1999-04-30
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 285
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-302-863-4

Query Match 93.4%; Score 1042.5; DB 11; Length 285;
 Best Local Similarity 76.5%; Pred. No. 7.7e-106;
 Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
 QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
 Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
 Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
 QY 88 GEGNSSONRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALE 145
 Db 121 GEGNSSONRNKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPMWLLSFKRGSALE 180
 QY 146 -----YQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQN----- 185
 Db 181 KENKILVKETGYFFIYQVLYTDKTYAMGHLIQKRVHVFQDELSTLFRCIQNMPETL 240
 QY 186 -----LEEGDELQALIPRENAQISLDGDTFFFGALKLL 218
 Db 241 PNNCYSAGIAKLEEGDELQALIPRENAQISLDGDTFFFGALKLL 285

RESULT 10
 US-09-880-748-3228
 ; Sequence 3228, Application US/09880748
 ; Publication No. US20030059937A1

GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3228
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3228

Query Match 93.4%; Score 1042.5; DB 11; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

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QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60

QY 45 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120

QY 88 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 145
Db 121 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

QY 146 -----YGVLYTDKTYAMGHLIQKRVHVFQGDLSLTVLFRCIQN----- 185
Db 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQKRVHVFQGDLSLTVLFRCIQNMPETL 240

QY 186 -----LEEGDELQAIAPRENAQISLDGDTFFFGALKLL 218
Db 241 PNNSCYSAGIAKLEEGDELQAIAPRENAQISLDGDTFFFGALKLL 285
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RESULT 11
US-09-932-613-173
; Sequence 173, Application US/09932613
; Publication No. US20030091565A1
GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-932-613-173

Query Match 93.4%; Score 1042.5; DB 11; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;

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Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60

QY 45 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120

QY 88 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 145
Db 121 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

QY 146 -----YGVLYTDKTYAMGHLIQKRVHVFQGDLSLTVLFRCIQN----- 185
Db 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQKRVHVFQGDLSLTVLFRCIQNMPETL 240

QY 186 -----LEEGDELQAIAPRENAQISLDGDTFFFGALKLL 218
Db 241 PNNSCYSAGIAKLEEGDELQAIAPRENAQISLDGDTFFFGALKLL 285
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RESULT 12

US-10-137-870-24
; Sequence 24, Application US/10137870
; Publication No. US20030138883A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C155
; CURRENT APPLICATION NUMBER: US/10/137,870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-24

Query Match 93.4%; Score 1042.5; DB 12; Length 285;

Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

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QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60

QY 45 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGA-----KIFEPPAP 87
Db 61 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120

QY 88 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 145
Db 121 GEGNSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
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Qy 146 -----YGOVLYTDKTYAMGHILQKRVHVFGEDELSTLTLFRCION----- 185
Db 181 KENKILVKETGYFFIYGOVLYTDKTYAMGHILQKRVHVFGEDELSTLTLFRCIONMPETL 240
Qy 186 -----LSEGEDELQAIAPRENAQISLDGVDVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQAIAPRENAQISLDGVDVTFFGALKLL 285

RESULT 13

US-10-140-018-24

; Sequence 24, Application US/10140018

; Publication No. US20030138885A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C158

; CURRENT APPLICATION NUMBER: US/10/140,018

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 24

; LENGTH: 285

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-140-018-24

Query Match 93.4%; Score 1042.5; DB 12; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

Qy 1 MDDSTEREQSRLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSRLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
Qy 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPAGKAGLEAPAVTAGLKIFEPAP 120

Qy 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALEE 145
Db 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALEE 180
Qy 146 -----YGOVLYTDKTYAMGHILQKRVHVFGEDELSTLTLFRCION----- 185
Db 181 KENKILVKETGYFFIYGOVLYTDKTYAMGHILQKRVHVFGEDELSTLTLFRCIONMPETL 240
Qy 186 -----LSEGEDELQAIAPRENAQISLDGVDVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQAIAPRENAQISLDGVDVTFFGALKLL 285

RESULT 14

US-10-140-021-24

; Sequence 24, Application US/10140021

; Publication No. US20030138886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-021-24

Query Match 93.4%; Score 1042.5; DB 12; Length 285;
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

Qy 1 MDDSTEREQSRLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSRLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
Qy 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPAP 87
Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPAGKAGLEAPAVTAGLKIFEPAP 120

Qy 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALEE 145
Db 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSFKRGSALEE 180
Qy 146 -----YGOVLYTDKTYAMGHILQKRVHVFGEDELSTLTLFRCION----- 185
Db 181 KENKILVKETGYFFIYGOVLYTDKTYAMGHILQKRVHVFGEDELSTLTLFRCIONMPETL 240
Qy 186 -----LSEGEDELQAIAPRENAQISLDGVDVTFFGALKLL 218
Db 241 PNNCSYAGIAKLEEGDELQAIAPRENAQISLDGVDVTFFGALKLL 285

RESULT 15

US-10-140-274-24

; Sequence 24, Application US/10140274

; Publication No. US20030143674A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C161
CURRENT APPLICATION NUMBER: US/10/140,274
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 24
LENGTH: 285
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-274-24

Query Match 93.4%; Score 1042.5; DB 12; Length 285;
Best Local Similarity 76.5%; Pred. No. 7, 7e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;
QY 1 MDDSTEREQSRLTSCCLKREMKLKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSRLTSCCLKREMKLKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGLASLRAELQGHAEKLPAG-----KIFEPAP 87
DB 61 LTVVSFYQVAALQGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL-- 145
DB 121 GEGNSSQNSRNKRAVQGPETVTQCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL 180
QY 146 -----YGVLYTDKTYAMGHILQKXKVVHVGDELSTLFRICION----- 185
DB 181 KENKILVKETGYFFTYGVLYTDKTYAMGHILQKXKVVHVGDELSTLFRICIONPETL 240
QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFEGALKLL 218
DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFEGALKLL 285

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Job time : 212.218 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 14.0489 Seconds
(without alignments)
656.548 Million cell updates/sec

Title: US-09-911-777-1

Perfect score: 1116

Sequence: 1 MDDSTEREQSLTSLCKRE.....ENAIQLDGDVTFFGALKLL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/aa/5B_COMB.pep:*
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- 4: /cgn2_6/ptodata/1/aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/aa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1042.5	93.4	285	US-09-286-529-1	Sequence 1, Appli
2	1042.5	93.4	285	US-09-589-287B-2	Sequence 2, Appli
3	1042.5	93.4	285	US-09-496-118B-1	Sequence 1, Appli
4	1042.5	93.4	285	US-09-565-423-2	Sequence 2, Appli
5	1042.5	93.4	285	US-09-879-919-23	Sequence 23, Appli
6	1042.5	93.4	285	US-09-588-947A-2	Sequence 2, Appli
7	927	83.1	266	US-09-589-287B-19	Sequence 19, Appli
8	927	83.1	266	US-09-879-919-24	Sequence 24, Appli
9	927	83.1	266	US-09-588-947A-19	Sequence 19, Appli
10	779.5	69.8	219	US-09-589-287B-28	Sequence 28, Appli
11	779.5	69.8	219	US-09-588-947A-28	Sequence 28, Appli
12	773.5	69.3	219	US-09-589-287B-30	Sequence 30, Appli
13	773.5	69.3	219	US-09-588-947A-30	Sequence 30, Appli
14	681	61.0	174	US-09-496-118B-5	Sequence 5, Appli
15	533	47.8	145	US-09-286-529-21	Sequence 21, Appli
16	523.5	46.9	289	US-09-589-287B-38	Sequence 38, Appli
17	523.5	46.9	289	US-09-588-947A-38	Sequence 38, Appli
18	379	34.0	155	US-09-589-287B-23	Sequence 23, Appli
19	379	34.0	155	US-09-588-947A-23	Sequence 23, Appli
20	196	17.6	46	US-09-496-118B-2	Sequence 2, Appli
21	152	13.6	250	US-08-883-086-2	Sequence 2, Appli
22	152	13.6	250	US-09-565-423-3	Sequence 3, Appli
23	151	13.5	205	US-09-286-529-5	Sequence 5, Appli
24	150	13.4	233	US-10-082-260-2	Sequence 2, Appli
25	150	13.4	233	US-08-815-783-2	Sequence 2, Appli
26	150	13.4	233	US-09-879-919-2	Sequence 2, Appli
27	150	13.4	250	US-09-153-927-4	Sequence 4, Appli

28 150 13.4 250 4 US-09-879-919-11 Sequence 11, Appli
29 144 12.9 234 4 US-09-157-864-2 Sequence 2, Appli
30 144 12.9 234 4 US-09-157-864-4 Sequence 4, Appli
31 142 12.7 234 4 US-09-879-919-13 Sequence 13, Appli
32 134 12.0 168 4 US-10-082-260-4 Sequence 4, Appli
33 134 12.0 168 4 US-08-815-783-4 Sequence 4, Appli
34 134 12.0 168 4 US-09-879-919-4 Sequence 4, Appli
35 126.5 11.3 147 3 US-08-883-086-3 Sequence 3, Appli
36 123 11.0 136 4 US-09-589-287B-20 Sequence 20, Appli
37 123 11.0 136 4 US-09-947A-20 Sequence 20, Appli
38 110 9.9 31 4 US-09-496-118B-3 Sequence 3, Appli
39 92.5 8.3 34 4 US-09-496-118B-4 Sequence 4, Appli
40 83.5 7.5 630 4 US-09-300-909-20 Sequence 20, Appli
41 83 7.4 384 4 US-09-648-004-6 Sequence 6, Appli
42 81.5 7.3 737 4 US-09-772-647-4 Sequence 4, Appli
43 80 7.2 261 3 US-08-961-083-164 Sequence 164, App
44 80 7.2 261 4 US-09-536-784-164 Sequence 164, App
45 78 7.0 281 3 US-09-118-408-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-286-529-1

; Sequence 1, Application US/09286529

; Patent No. 6297367

; GENERAL INFORMATION:

; APPLICANT: Catherine Tribouley

; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES

; FILE REFERENCE: 1408.003/200130.439C1

; CURRENT APPLICATION NUMBER: US/09/286.529

; CURRENT FILING DATE: 1999-04-05

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 285

; TYPE: PRT

; ORGANISM: human

US-09-286-529-1

Query Match 93.4%; Score 1042.5; DB 3; Length 285;

Best Local Similarity 76.5%; Pred. No. 5.4e-118;

Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY	1	MDDSTEREQSLTSLCKREEMKKECVSIIPRKESPSVRSKDGKLLAATLLALLSCC	44	-----LLSCC
DB	1	MDDSTEREQSLTSLCKREEMKKECVSIIPRKESPSVRSKDGKLLAATLLALLSCC	60	-----KIFEPPAP
QY	45	LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP	87	-----KIFEPPAP
DB	61	LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP	120	-----KIFEPPAP
QY	88	CEGSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQGSIYTFVPWLLSFKRGSL--	145	-----KIFEPPAP
DB	121	CEGSSQNSNRKRAVQGPETVTQDCLQIADSETPTIQGSIYTFVPWLLSFKRGSALEE	180	-----KIFEPPAP
QY	146	-----YGVLYTDKTYAMGHILQKRVHVFQDGLSLVTLFRCIQ-----	185	-----KIFEPPAP
DB	181	KENKILVKETGYFTYGVLYTDKTYAMGHILQKRVHVFQDGLSLVTLFRCIQMPETL	240	-----KIFEPPAP
QY	186	-----LEEGDLSLQAIIPRENAQISLDGDVTFFGALKLL	218	-----KIFEPPAP
DB	241	PNNCSYAGIAKLEGEDELQAIIPRENAQISLDGDVTFFGALKLL	285	-----KIFEPPAP

RESULT 2

US-09-589-287B-2

; Sequence 2, Application US/09589287B

; Patent No. 6403770

; GENERAL INFORMATION:

; APPLICANT: Yu et al.

; TITLE OF INVENTION: Antibodies to Neutrokine-alpha

```

; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-589-287B-2

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Query Match	93.4%	Score 1042.5;	DB 4;	Length 285;
Best Local Similarity	76.5%;	Pred. No. 5.4e-118;		
Matches 218; Conservative	0;	Mismatches 0;	Indels 67;	Gaps 4;

QY	1	MDDSTEREQSLTSCCLKREEMKKECVSILPKRSPSV-----LLSCC	44
DB	1	MDDSTEREQSLTSCCLKREEMKKECVSILPKRSPSVSSDKGLLAATLLALLSCC	60
QY	45	LTVVSFYQVAALQGDLASLRAELQGHHAELKPAGA-----KIFEPAP	87
DB	61	LTVVSFYQVAALQGDLASLRAELQGHHAELKPAGAPKAGLEAPAVTAGLKIFEPAP	120
QY	88	GEGNSSQNSRNKRAVGQPEETVTQDCLQIADSEPTTIQKGSYTFVPLLSPKRGSALE--	145
DB	121	GEGNSSQNSRNKRAVGQPEETVTQDCLQIADSEPTTIQKGSYTFVPLLSPKRGSALEE	180
QY	146	-----YGOVLVTDKTYAMGHLIQRKKVHVFGDELSLVTLCFRICQN-----	185
DB	181	KENKILVKETGYFYIYGOVLVTDKTYAMGHLIQRKKVHVFGDELSLVTLCFRICQNMPEYL	240
QY	186	-----LEEGDELQLAIPRENAQISLDGVDVTFPGALKLL	218
DB	241	PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVDVTFPGALKLL	285

US-09-565-423-2	SEQUENCE 2, APPLICATION US/09565423
PATENT NO. 6475987	PATENT NO. 6475987
GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: SHU, HONG-BING	APPLICANT: SHU, HONG-BING
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND METHODS OF USE THEREOF	TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND METHODS OF USE THEREOF
FILE REFERENCE: 2879-72	FILE REFERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/09/565,423	CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05	CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: UNKNOWN	PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR FILING DATE: 2000-05-01	PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/132,892	PRIOR APPLICATION NUMBER: 60/132,892
PRIOR FILING DATE: 1999-05-06	PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17	NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1	SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2	SEQ ID NO 2
LENGTH: 285	LENGTH: 285
TYPE: PRT	TYPE: PRT
ORGANISM: Artificial Sequence	ORGANISM: Artificial Sequence
FEATURE:	FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer	OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-565-423-2	US-09-565-423-2

```

RESULT 3
US-09-496-118B-1
; Sequence 1, Application US/09496118B
; Patent No. 6475986
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat B.
; TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
; TITLE OF INVENTION: Apoptosis
; FILE REFERENCE: D6206
; CURRENT APPLICATION NUMBER: US/09/496,118B
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 60/118,531
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 1
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: amino acid sequence of THANK protein
US-09-496-118B-1

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Query Match	93.4%;	Score 1042.5;	DB 4;	Length 285;	
Best Local Similarity	76.5%;	Pred. No. 5.4e-118;			
Matches 218;	Conservative 0;	Mismatches 0;	Indels 67;	Gaps 4;	
Qy	1	MDSTEREQSRLTSLCKKEEMKLEKCVSILPRKSPSV-----LISCC 44			
Dd	1	MDSTEREQSRLTSLCKKEEMKLEKCVSILPRKSPSVRRSSDKGKLAAATILLALLISCC 60			
Qy	45	LTVVSFYQAALQGDLASLRRAELQGHHAEPKLPGA-----KIFEPAP 87			
Dd	61	LTVVSFYQAALQGDLASLRRAELQGHHAEPKLPAGAPAKGLEEAPAVTAGIKIFEPAP 120			
Qy	88	GEGNSSQNRNKAAGVPETVTQDCLQLIASSETPTTKGSYTFVPMLLSFKGKSAL-- 145			

;; PRIOR APPLICATION NUMBER: 60/277,978
;; PRIOR FILING DATE: 2001-03-23
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/254,875
;; PRIOR FILING DATE: 2000-12-13
;; PRIOR APPLICATION NUMBER: 60/241,952
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/211,537
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 08/815,783
;; PRIOR FILING DATE: 1997-03-12
;; PRIOR APPLICATION NUMBER: 60/016,812
;; PRIOR FILING DATE: 1996-03-14
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 23
;; LENGTH: 285
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-879-919-23

Query Match 93.4%; Score 1042.5; DB 4; Length 285;
Best Local Similarity 76.5%; Pred. No. 5.4e-118;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVSSKDGKLLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPAGAEAPAVTAGLKIFEPPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL-- 145
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL 180
QY 146 -----YGOVLYTDKTYAMGHLLQKRVHVFVFGDELSTLTLFRICQN----- 185
DB 181 KENKILVKETGYFFYGVQVLYTDKTYAMGHLLQKRVHVFVFGDELSTLTLFRICQNMPETL 240
QY 186 -----LEEDELQLAIPRENAQISLDGDVTFPGALKLL 218
DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDVTFPGALKLL 285

RESULT 6
US-09-588-947A-2
;; Sequence 2, Application US/09588947A
;; Patent No. 6562579
;; GENERAL INFORMATION:
;; APPLICANT: Yu et al.
;; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokine-alpha
;; FILE REFERENCE: PF343P3C2
;; CURRENT APPLICATION NUMBER: US/09/588,947A
;; CURRENT FILING DATE: 2000-06-08
;; PRIOR APPLICATION NUMBER: 09/588,947
;; PRIOR FILING DATE: 2000-06-08
;; PRIOR APPLICATION NUMBER: 09/507,968
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: 60/122,388
;; PRIOR FILING DATE: 1999-03-02
;; PRIOR APPLICATION NUMBER: 60/124,097
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 60/126,599
;; PRIOR FILING DATE: 1999-03-26
;; PRIOR APPLICATION NUMBER: 60/127,598
;; PRIOR FILING DATE: 1999-04-02
;; PRIOR APPLICATION NUMBER: 60/130,412
;; PRIOR FILING DATE: 1999-04-16
;; PRIOR APPLICATION NUMBER: 60/130,696
;; PRIOR FILING DATE: 1999-04-23

;; PRIOR APPLICATION NUMBER: 60/131,278
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131,673
;; PRIOR FILING DATE: 1999-04-29
;; PRIOR APPLICATION NUMBER: 60/136,784
;; PRIOR FILING DATE: 1999-05-28
;; PRIOR APPLICATION NUMBER: 60/142,659
;; PRIOR FILING DATE: 1999-07-06
;; PRIOR APPLICATION NUMBER: 60/145,824
;; PRIOR FILING DATE: 1999-07-27
;; PRIOR APPLICATION NUMBER: 60/167,239
;; PRIOR FILING DATE: 1999-11-24
;; PRIOR APPLICATION NUMBER: 60/168,624
;; PRIOR FILING DATE: 1999-12-03
;; PRIOR APPLICATION NUMBER: 60/171,108
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: 60/171,626
;; PRIOR FILING DATE: 1999-12-23
;; PRIOR APPLICATION NUMBER: 60/176,015
;; PRIOR FILING DATE: 2000-01-14
;; PRIOR APPLICATION NUMBER: 09/255,794
;; PRIOR FILING DATE: 1999-02-23
;; PRIOR APPLICATION NUMBER: 09/005,874
;; PRIOR FILING DATE: 1998-01-12
;; PRIOR APPLICATION NUMBER: 60/036,100
;; PRIOR FILING DATE: 1997-01-14
;; PRIOR APPLICATION NUMBER: PCT/US96/17957
;; PRIOR FILING DATE: 1996-10-25
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 285
;; TYPE: PRT
;; ORGANISM: human
US-09-588-947A-2

Query Match 93.4%; Score 1042.5; DB 4; Length 285;
Best Local Similarity 76.5%; Pred. No. 5.4e-118;
Matches 218; Conservative 0; Mismatches 0; Indels 67; Gaps 4;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSV-----LLSCC 44
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVSSKDGKLLAATLLALLSCC 60
QY 45 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGA-----KIFEPPAP 87
DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPAGAEAPAVTAGLKIFEPPAP 120
QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL-- 145
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSAL 180
QY 146 -----YGOVLYTDKTYAMGHLLQKRVHVFVFGDELSTLTLFRICQN----- 185
DB 181 KENKILVKETGYFFYGVQVLYTDKTYAMGHLLQKRVHVFVFGDELSTLTLFRICQNMPETL 240
QY 186 -----LEEDELQLAIPRENAQISLDGDVTFPGALKLL 218
DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDVTFPGALKLL 285

RESULT 7
US-09-589-287B-19
;; Sequence 19, Application US/09589287B
;; Patent No. 6403770
;; GENERAL INFORMATION:
;; APPLICANT: Yu et al.
;; TITLE OF INVENTION: Antibodies to Neutrokine-alpha
;; FILE REFERENCE: PF343P3C1
;; CURRENT APPLICATION NUMBER: US/09/589,287B
;; CURRENT FILING DATE: 2000-06-08
;; Prior application data removed - check PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 42

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-19

Query Match      83.1%; Score 927; DB 4; Length 266;
Best Local Similarity 69.8%; Pred. No. 5e-104;
Matches 199; Conservative 0; Mismatches 0; Indels 86; Gaps 5;

QY 1 MDDSTEREQSLTSCCKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCKREEMKKECVSILPRKESPSVRSKDGKGLLAATLLALLSCC 60

QY 45 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGA-----KIFEPAP 87
Db 61 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120

QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKGYTFVPMWLLSFKRGSALEE 145
Db 121 GEGNSSQNSRNKRAVQGPET-----GSYTFVPMWLLSFKRGSALEE 161

QY 146 -----YQGVLYTDKTYAMGHLIQKRVHVFQDELSLVTFLFCION----- 185
Db 162 KENKILVKETGYFFIYQGVLYTDKTYAMGHLIQKRVHVFQDELSLVTFLFCIONMPETL 221

QY 186 -----LEEGDELQALAI PRENAQISLDGDTFFFGALKLL 218
Db 222 PNNCSYAGIAKLEEGDELQALAI PRENAQISLDGDTFFFGALKLL 266

RESULT 8
US-09-879-919-24
; Sequence 24, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-24

Query Match      83.1%; Score 927; DB 4; Length 266;
Best Local Similarity 69.8%; Pred. No. 5e-104;
Matches 199; Conservative 0; Mismatches 0; Indels 86; Gaps 5;

QY 1 MDDSTEREQSLTSCCKREEMKKECVSILPRKESPSV-----LLSCC 44
Db 1 MDDSTEREQSLTSCCKREEMKKECVSILPRKESPSVRSKDGKGLLAATLLALLSCC 60

QY 45 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGA-----KIFEPAP 87
Db 61 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120

QY 88 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKGYTFVPMWLLSFKRGSALEE 145
Db 121 GEGNSSQNSRNKRAVQGPET-----GSYTFVPMWLLSFKRGSALEE 161

QY 146 -----YQGVLYTDKTYAMGHLIQKRVHVFQDELSLVTFLFCION----- 185
Db 162 KENKILVKETGYFFIYQGVLYTDKTYAMGHLIQKRVHVFQDELSLVTFLFCIONMPETL 221

QY 186 -----LEEGDELQALAI PRENAQISLDGDTFFFGALKLL 218
Db 222 PNNCSYAGIAKLEEGDELQALAI PRENAQISLDGDTFFFGALKLL 266

RESULT 9
US-09-588-947A-19
; Sequence 19, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-588-947A-19

  Query Match      83.1%; Score 927; DB 4; Length 266;
  Best Local Similarity 69.8%; Pred. No. 5e-104;
  Matches 199; Conservative 0; Mismatches 0; Indels 86; Gaps 5;

QY 1 MDDSTEREOSRLTSLCKREEMKLEKCVSILPRKESPSV-----LLSCC 44
    |||||
Db 1 MDDSTEREOSRLTSLCKREEMKLEKCVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
    |||||
QY 45 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAE-----KIFEPAP 87
    |||||
Db 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAEAPAVTAGLKIFEPAP 120
    |||||
QY 88 GEGNSSONSRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSPKRGSA-- 145
    |||||
Db 121 GEGNSSONSRKRAVQGPET-----GSYTFVPWLLSPKRGSALEE 161
    |||||
QY 146 -----YGVLYTDKTYAMGHLLQKRVHVGDELSTLTLFRCIQ----- 185
    |||||
Db 162 KENKILVKETGYFFYTGQVLYTDKTYAMGHLLQKRVHVGDELSTLTLFRCIQNPETL 221
    |||||
QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 218
    |||||
Db 222 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 266
    |||||

RESULT 10
US-09-589-287B-28
; Sequence 28, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; PRIOR FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-28

  Query Match      69.8%; Score 779.5; DB 4; Length 219;
  Best Local Similarity 74.0%; Pred. No. 3e-86;
  Matches 162; Conservative 3; Mismatches 3; Indels 51; Gaps 3;

QY 51 YQVAALQGDLSLRAELQGHHAELKLP-----AGAKIFEPAPGEGNSS 93
    |||||
Db 1 YQVAAVQGDLSLRAELQGHHAELKLPARAPAKAGLGEAPAVTAGLKIFEPAPGEGNSS 60
    |||||
QY 94 QNSNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSPKRGSA-- 145
    |||||
Db 61 QSSNRKRAIQGAETVIQDCLQIADSETPTIQKSYTFVPWLLSPKRGSALEEKENKIL 120
    |||||
QY 146 -----YGVLYTDKTYAMGHLLQKRVHVGDELSTLTLFRCIQ----- 185
    |||||
Db 121 VKETGYFFYTGQVLYTDKTYAMGHLLQKRVHVGDELSTLTLFRCIQNPETLNNSCY 180
    |||||
QY 186 -----LEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 218
    |||||
Db 181 SAGIAKLEEGDELQLAIPRENAQISLDGVDVTFPGALKLL 219
    |||||

RESULT 11
US-09-588-947A-28
; Sequence 28, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-588-947A-28

  Query Match      69.8%; Score 779.5; DB 4; Length 219;
  Best Local Similarity 74.0%; Pred. No. 3e-86;
  Matches 162; Conservative 3; Mismatches 3; Indels 51; Gaps 3;

QY 51 YQVAALQGDLSLRAELQGHHAELKLP-----AGAKIFEPAPGEGNSS 93
    |||||
Db 1 YQVAAVQGDLSLRAELQGHHAELKLPARAPAKAGLGEAPAVTAGLKIFEPAPGEGNSS 60
    |||||
QY 94 QNSNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSPKRGSA-- 145
    |||||
Db 61 QSSNRKRAIQGAETVIQDCLQIADSETPTIQKSYTFVPWLLSPKRGSALEEKENKIL 120
    |||||
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Qy 146 -----YQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRICION----- 185
Db 121 VKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRICIONMPETLPNNSCY 180
Qy 186 -----LEEGDELOLAIPRENAQISLDGDTFFGALKLL 218
Db 181 SAGIAKLEEGDELOLAIPRENAQISLDGDTFFGALKLL 219

RESULT 12
US-09-589-287B-30
; Sequence 30, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-30

Query Match 69.3%; Score 773.5; DB 4; Length 219;
Best Local Similarity 73.5%; Pred. No. 1.6e-85;
Matches 161; Conservative 3; Mismatches 4; Indels 51; Gaps 3;

Qy 51 YQVAALQGDLSLRAELQGHAEKLP-----AGAKIFEPAPGEGNSS 93
Db 1 YQVAAVQGDLSLRAELQGHAEKLPARAPAKAGLGEAPAVTAGLKIFEPAPGEGNSS 60
Qy 94 QNSNRKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPMWLSFKRGSAL----- 145
Db 61 QSSNRKRAIQAEETVIQDCLQLIADSETPTIQKGSYTFVPMWLSFKRGSALKEENKIL 120
Qy 146 -----YQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRICION----- 185
Db 121 VKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRICIONMPETLPNNSCY 180
Qy 186 -----LEEGDELOLAIPRENAQISLDGDTFFGALKLL 218
Db 181 SAGIAKLEEGDELOLAIPRENAQISLDGDTFFGALKLL 219

RESULT 13
US-09-588-947A-30
; Sequence 30, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
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; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-588-947A-30

Query Match 69.3%; Score 773.5; DB 4; Length 219;
Best Local Similarity 73.5%; Pred. No. 1.6e-85;
Matches 161; Conservative 3; Mismatches 4; Indels 51; Gaps 3;

Qy 51 YQVAALQGDLSLRAELQGHAEKLP-----AGAKIFEPAPGEGNSS 93
Db 1 YQVAAVQGDLSLRAELQGHAEKLPARAPAKAGLGEAPAVTAGLKIFEPAPGEGNSS 60
Qy 94 QNSNRKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPMWLSFKRGSAL----- 145
Db 61 QSSNRKRAIQAEETVIQDCLQLIADSETPTIQKGSYTFVPMWLSFKRGSALKEENKIL 120
Qy 146 -----YQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRICION----- 185
Db 121 VKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRICIONMPETLPNNSCY 180
Qy 186 -----LEEGDELOLAIPRENAQISLDGDTFFGALKLL 218
Db 181 SAGIAKLEEGDELOLAIPRENAQISLDGDTFFGALKLL 219

RESULT 14
US-09-496-118B-5
; Sequence 5, Application US/09496118B
; Patent No. 6475986
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat B.
; TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
; TITLE OF INVENTION: Apoptosis
; FILE REFERENCE: D6206
; CURRENT APPLICATION NUMBER: US/09/496,118B
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 60/118,531
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 13
```

```
; SEQ ID NO 5
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: domain
; LOCATION: 112..285
; OTHER INFORMATION: sequence of THANK extracellular domain
US-09-496-118B-5

Query Match      61.0%; Score 681; DB 4; Length 174;
Best Local Similarity 80.3%; Pred. No. 1.9e-74;
Matches 139; Conservative 0; Mismatches 0; Indels 34; Gaps 2;

QY 80 KIFEPPAPGEGNSSQNRKRAVQGPETVTQDCLQLIADSETPTIQGSYTFVPWLLSF 139
Db 2 KIFEPPAPGEGNSSQNRKRAVQGPETVTQDCLQLIADSETPTIQGSYTFVPWLLSF 61

QY 140 KRGSAL-----YQGVLYTDKTYAMGHILQKKVHVFGDELSLVTLPFC 182
Db 62 KRGSALEEKENKILVKETGYFFIYQGVLYTDKTYAMGHILQKKVHVFGDELSLVTLPFC 121

QY 183 ION-----LEEGDELAIPRENAQISLDGDTFFFGALKLL 218
Db 122 IQNMPETLPNNSCYSAGIAKLEEGDELAIPRENAQISLDGDTFFFGALKLL 174
```

```
RESULT 15
US-09-286-529-21
; Sequence 21, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Triboulev
; TITLE OF INVENTION: NEW MEMBERS OF TNP AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-21
```

```
Query Match      47.8%; Score 533; DB 3; Length 145;
Best Local Similarity 76.6%; Pred. No. 1.3e-56;
Matches 111; Conservative 0; Mismatches 0; Indels 34; Gaps 2;

QY 108 TVTQDCLQLIADSETPTIQGSYTFVPWLLSFKRGSA-----YQGVYL 150
Db 1 TVTQDCLQLIADSETPTIQGSYTFVPWLLSFKRGSALEKENKILVKETGYFFIYQGVYL 60

QY 151 YTDKTYAMGHILQKKVHVFGDELSLVTLPFCION-----LEEGDELAQ 193
Db 61 YTDKTYAMGHILQKKVHVFGDELSLVTLPFCIONMPETLPNNSCYSAGIAKLEEGDELAQ 120

QY 194 LAIPRENAQISLDGDTFFFGALKLL 218
Db 121 LAIPRENAQISLDGDTFFFGALKLL 145
```

Search completed: February 3, 2004, 07:44:54
Job time : 16.0489 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	85	7.1	767	2	I51083	SOX-LZ - rainbow t
2	84.5	7.0	380	2	A70646	probable PPE prote
3	82.5	6.9	1153	2	T26883	hypothetical prote
4	81.5	6.8	1121	2	C87973	protein V43P6C.12
5	81	6.7	449	1	A38449	regulatory protein
6	81	6.7	891	2	T25714	hypothetical protei
7	80.5	6.7	1735	2	A57607	Munc11-1 - rat
8	80	6.6	613	2	S27770	hypothetical prote
9	80	6.6	842	2	T41697	translation elonga
10	79.5	6.6	573	2	H90726	probable secD - My
11	78.5	6.5	313	2	B96037	alpha-galactoside
12	78.5	6.5	498	1	VG8EGX	secreted glycoprot
13	78.5	6.5	737	2	S72442	actin-fragmin kina
14	78.5	6.5	1015	2	C84918	probable ATP-depen
15	78.5	6.5	15281	2	A41309	claglosporin synthe
16	78	6.5	373	2	A97426	flagellar P-ring p
17	78	6.5	373	2	A12643	flagellar P-ring p
18	78	6.5	391	2	C84268	aspartate aminotra
19	77.5	6.4	383	1	VG8EGK	glycoprotein precu
20	77.5	6.4	404	2	B85466	hypothetical prote
21	77.5	6.4	434	2	T20400	hypothetical prote
22	77.5	6.4	454	2	A56954	yes-associated pro
23	77.5	6.4	920	2	C98831	hypothetical prote
24	77	6.4	2399	2	AH3009	non-ribosomal pept
25	77	6.4	2399	2	F98274	hypothetical prote
26	77	6.4	3005	1	GNVSTV	genome polypeptide
27	76.5	6.4	218	2	A96831	hypothetical prote
28	76.5	6.4	882	2	T43250	spindle pole body-
29	76.5	6.4	1070	2	T05733	kinin homolog F2


```
A:Molecule type: mRNA
A:Residues: 1-1735 <RES>
A:Cross-references: EMBL:U24070; NID:g915327; PIDN:AAC52266.1; PID:g915328
C:Superfamily: protein kinase C zinc-binding repeat homology
F:567-616/Domain: protein kinase C zinc-binding repeat homology <KZ2>
```

		Query Match	6.7%; Score 80.5; DB 2; Length 1735;
		Best Local Similarity	23.3%; Pred. No. 85;
		Matches 47; Conservative 26; Mismatches 58; Indels 71; Gaps 12;	
Qy	19	KGED-MKVGYDPTTPQK--EEGAVL-LSSSFAM-----SLYQLALQAOLDMLRME	66
Dd	858	KGDADMKVYYDE-TAQEIYDEFAMRYGVESIYAQMTHFACLSKYMCPCGPVPAYMSTLLAN	916
Qy	67	LQSYRGSAIPAA-----AKLLTPAAPRHNSR---GHENRRAFP	104
Dd	917	INAYAHHTASTNVASDRPASNFGERFKVL----DLHNLSDIDLISWYNRNFPASS	972
Qy	105	PPEEQDV-----DLSAPPALRNIIODCLLIADSPDTPIRKGYTYF	146
Dd	973	PERL-QDLKSTVDLLTSITFERMKVGLOQPSPRASQVVXDKVCACLNS-----TYEY	1023
Qy	147	VPWLSSFKKGNALYSQVLYTDP	168
Dd	1024	I-----FNHCHELYGREYOTDP	1040

```

RESULT 8
S27770
  hypothetical protein 1 - African malaria mosquito (fragment)
C:Species: Anopheles gambiae (African malaria mosquito)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C:Accession: S27770
R:Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H.
  submitted to the EMBL Data Library, June 1992
A:Description: Distinct families of site-specific retroposons occupy identical
A:Reference number: S27770
A:Accession: S27770
A:Molecule type: DNA
A:Residues: 1-613 <BES>
A:Cross-references: EMBL:M93690; NID:gl59615; PID:gl59616

      Query Match          6.6%; Score 80; DB 2; Length 613;
      Best Local Similarity 29.2%; Pred. No. 25;
      Matches 35; Conservative 16; Mismatches 37; Indels 32; Gaps 6;

QY 17 SKKGEDMKV-----GYDPTTPQKEGAVLLSSSFATMSLYQLA-----AL 56

```

Db	109	SOOREEMTYPATSTPKAGKCSAEPSELSENNESLKLL-----AMQVAQLSLKSLCKREL	163
Qy	57	QADLMN---LRMELQSYRGSAATPAAAKLLTPAAPRPHNSSRG--HNRRAFPGPPEETEQ	110
Db	164	QESLMKNAALERELETYRMGAR-SVIELOQQAAAAAPMTAQGAHSSNRNRGRGPGPOOQE	222

RESULT 9

T41697

translation elongation factor eEF-2 [similarity] - fission yeast (Schizosacchar

C:Species: Schizosaccharomyces pombe

C:Accession: U41697, U139236, U38996, U51994, U42427
 R:Wedler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, August 1999
 A:Reference number: Z22010
 A:Accession: T41697
 A:Molecule type: DNA
 A:Residues: 1-842 *WED>
 A:Cross-references: EMBL:AL121859; PIDN:CA858373.1; GSPDB:GNO0068; SPDB:SPCP31B
 A:Experimental source: strain 972H; clone p1 p31B10
 A:Genetics: SP2
 R:Stevens, K.; Churcher, C.; McDougall, R.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, August 1999
 A:Reference number: Z21838

Db 736 SENAMGIYSVLNKRGHVFSSE 758

RESULT 10

B70726

probable secD - Mycobacterium tuberculosis (strain H37RV)

C/Species: Mycobacterium tuberculosis

C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C/Accession: B70726

R;Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: B70726

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-573 <COL>

A;Cross-references: GB:Z77724; GB:AL123456; NID:G3261620; PIDN:CAB01256.1; PID:g1478225

A;Experimental source: strain H37RV

C/Genetics:

A;Gene: secD

C;Superfamily: protein export membrane protein secD

Query Match 6.6%; Score 79.5; DB 2; Length 573;

Best Local Similarity 22.3%; Pred. No. 26;

Matches 46; Conservative 23; Mismatches 80; Indels 57; Gaps 9;

QY 74 ATPAAKLLTPAAPRHNSRGHRNRAPPGPEETEQDVLSAPPA----- 119

Db 149 AAPPAAQSGAPSPQGAQPRYPQDPA-PSNPSTSPASFPAPPAEAPATDPKDLAER 207

QY 120 -----LRNIIDQCLOLI-----AUSDTP-----TIRKGYTFYPWL 150

Db 208 IAEKRLQSTNQYMQWVALQFQATRCSDDDILGNDPDKPLVTCSDHKTAYLLAPSI 267

QY 151 LSPKRGNALYSQVLYTDPIFAMGHVQIRK---KVHVFQD-----ELSLVTLFRICQMLEE 202

Db 268 IS---GQIQNATSGMDQ-RGIGYVVDIQFKGPAANIWADYTAAHICTQTAFILDSQVVS 323

QY 203 GDEIQLAIPRENAQISRNGDDTFFGA 228

Db 324 APQIQEALPGGRTQIS-GGDPPPTAA 348

RESULT 11

H96037

alpha-galactoside utilization transcription regulator, Arac family protein [imported] -

C/Species: Sinorhizobium meliloti

C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C/Accession: H96037

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: H96037

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-313 <KUR>

A;Cross-references: GB:AL51985; PIDN:CAC49968.1; PID:g15141456; GSPDB:GN00167

A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaunt, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C/Genetics:

A:Gene: gqpt; Smb21649
A:Genome: plasmid

Query Match 6.5%; Score 78.5; DB 2; Length 313;
Best Local Similarity 25.0%; Pred. No. 15;
Matches 38; Conservative 20; Mismatches 43; Indels 51; Gaps 8;

QY 62 NLRLMEQSYRGSGATPAAAKLLTPAAPRPHN-----SSRGHNR 99
DB 69 NLRYENRTHR--VRPGETILLV-----PHNRYWLEGGRGWFFWISMGEEALRIHRAI 122
QY 100 RAPPGPEETEODVDLSAPALRNIIQDCLQIADSTPTIRKGTTFVFWLLSFKRGNAL 159
DB 123 LAVTGPITLIQ-----PDTVEHLADCSRLIAGGETP-----ATAYEAAMAL 168
QY 160 YSOVLVTDPIFA-----MGHVIQKKVHVFGD 186
DB 169 YDDVFGSHVSLVEEYRKMQHVID-----HILGN 196

RESULT 12

VGBEGX

secreted glycoprotein gX - suid herpesvirus 1

C:Species: suid herpesvirus 1
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
C:Accession: A21879
R:Rea, T.J.; Timmins, J.G.; Long, G.W.; Post, L.E.
J. Virol. 54, 21-29, 1985
A:Title: Mapping and sequence of the gene for the pseudorabies virus glycoprotein which
A:Reference number: A21879; MUID:85135070; PMID:2983115
A:Accession: A21879
A:Molecule type: DNA
A:Residues: 1-498 <REA>
A:Cross-references: GB:M10986; NID:G334060; PIDN:AAC35206.1; PID:G334061
C:Superfamily: pseudorabies virus glycoprotein gX
C:Keywords: glycoprotein
F:56,86,142,226,443/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.5%; Score 78.5; DB 1; Length 498;
Best Local Similarity 25.3%; Pred. No. 27;
Matches 55; Conservative 26; Mismatches 73; Indels 63; Gaps 12;

QY 15 FCEKGEKMGVYDPTTPQ-----KEGAVLLSSFTMSLYQLAA----- 55
DB 247 FRSESDDEVHGDAPPAEGEETEEAEELTSSDLNIEVVGSPAAPAEGPATEEGRG 306
QY 56 -----LOADMLNRLMEQSYRGSGATPAAAKLLTPAAPRPHNSRGH-----RNRAPP 103
DB 307 ABEDELTSDDLNIIEVYV-----GSPRPASS-PPPPPPRPHPRGRDHDHGHRRADDR 362
QY 104 GPEETEODVDLSAPALRNIIQDCLQIADSD---TPTIRKGTTFVFWLLSFKRGNAL 160
DB 363 GQORHR-----LPPE-----PTFVSPSDFVTPT---GS-----PALLGLGSLA 402
QY 161 SOVLVTDPIFAMGHV---IQKKVHV---FGDELSLV 192
DB 403 SRPHLTAGTGAQHVEAQKSRHRSGLGLQLSVET 439

RESULT 13

S72442

actin-fragmin kinase - slime mold (Physarum polycephalum)

C:Species: Physarum polycephalum
C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 29-Oct-1999
C:Accession: S72442; S78484
R:Richinger, L.; Bombli, L.; Vandekerckhove, J.; Schleicher, M.; Gettemans, J.
EMBO J. 15, 5547-5556, 1996
A:Title: A novel type of protein kinase phosphorylates actin in the actin-fragmin complex
A:Reference number: S72442; MUID:97051813; PMID:8996448
A:Accession: S72442
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-737 <BICI>

A:Cross-references: EMBL:U64722; NID:G1553132; PIDN:AAB08728.1; PID:G1553133
A:Accession: S78484
A:Molecule type: protein
A:Residues: 13-20; 43-49; 68-73; 206-209; 214-223; 235-248; 250-262; 410-420; 443-454; 459-470; 474-484
A:Note: 560-Lys was also found
C:Function:
A:Description: phosphorylates specifically actin in the EGTA-resistant actin-fragmin complex

Query Match 6.5%; Score 78.5; DB 2; Length 737;
Best Local Similarity 21.1%; Pred. No. 44;
Matches 39; Conservative 31; Mismatches 56; Indels 59; Gaps 9;

QY 26 GYDPTTPQKEGAVLLSSSFTA-----MSLYQALQADLMNLRMELQ-----SYRGSATP 76
DB 278 GYDVCT-----EGSISMQSGFLATVRECAFDLDAFERELLSWQESLKQCHNLSISQAIP 333
QY 77 AAALL-----TPAAPRPHNSRGHNRRAFPDPPEETEODVDL-----SA 116
DB 334 FILRLRIFPHDAIHNPSPSPSPSS-----SSSTSHPTPASSSTSTLSPSSIPSSNTSP 390
QY 117 PPALRN-----IODC--LQIADSTPTIRKGTTFVFWLLSFKRGNALYSOVLVTDPIF 170
DB 391 PPASSESLVGVCECAWLKVVVPNEKPAPRR-----YHGVLYEGKLY 433
QY 171 AMGHV 175
DB 434 VEGGV 438

RESULT 14

C84918

probable ATP-dependent RNA helicase A [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84918
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84918
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-1015 <SOT>
A:Cross-references: GB:AEO02093; NID:G3738282; PIDN:AAC63624.1; GSPDB:GNO0139
C:Genetics:
A:Gene: At2g47680
A:Map position: 2

Query Match 6.5%; Score 78.5; DB 2; Length 1015;
Best Local Similarity 29.5%; Pred. No. 66;
Matches 23; Conservative 15; Mismatches 29; Indels 11; Gaps 5;

QY 103 PGPETEODVLSAPPALRNIIQDCLQIADSTPTIRKGTTFVFWLLSFKRGNALYSQ 162
DB 236 PGPSPSSADTEIK--PELQNLHDLILYHEKE-PDIEKSLVFLPTYSLEQ---QYHQ 289
QY 163 VLYTDPIFAM--GHVIR 178
DB 290 L---EPFFASPEVHILHR 304

RESULT 15

S41309

cyclosporin synthetase - cyclosporin fungus

C:Species: Tolypocladium inflatum (cyclosporin fungus)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-Nov-2000
C:Accession: S45487; S41309
R:Weber, G.; Schoengendorfer, K.; Schneider-Scherzer, E.; Leitner, E.
Curr. Genet. 26, 120-125, 1994
A:Title: The peptide synthetase catalyzing cyclosporine production in Tolypocladium nive
A:Reference number: S45487; MUID:95094306; PMID:8001164

A:Accession: S45487
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-15281 <WEB>
A:Cross-references: EMBL:Z28383; NID:G440168; PIDN:CAA82227.1; PID:G440169
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
A>Note: only a part of the translation is shown
A>Note: the source is designated as *Tolypocladium inflatum*
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: cyclosporin fungus cyclosporin synthetase; acetate-CoA ligase homology; a
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
F:532-1008/Domain: acetate-CoA ligase homology <ACLI>
F:1029-1096/Domain: acyl carrier protein homology <ACP1>
F:1618-2069/Domain: acetate-CoA ligase homology <ACL2>
F:2527-2594/Domain: acyl carrier protein homology <ACP2>
F:3115-3553/Domain: acetate-CoA ligase homology <ACL3>
F:4014-4081/Domain: acyl carrier protein homology <ACP3>
F:4601-5057/Domain: acetate-CoA ligase homology <ACL4>
F:5506-5573/Domain: acyl carrier protein homology <ACP4>
F:6094-6546/Domain: acetate-CoA ligase homology <ACL5>
F:7003-7070/Domain: acyl carrier protein homology <ACP5>
F:7591-8042/Domain: acetate-CoA ligase homology <ACL6>
F:8063-8130/Domain: acyl carrier protein homology <ACP6>
F:8652-9157/Domain: acetate-CoA ligase homology <ACL7>
F:9558-9625/Domain: acyl carrier protein homology <ACP7>
F:10146-10586/Domain: acetate-CoA ligase homology <ACL8>
F:11055-11122/Domain: acyl carrier protein homology <ACP8>
F:11635-12106/Domain: acetate-CoA ligase homology <ACL9>
F:12127-12194/Domain: acyl carrier protein homology <ACP9>
F:12715-13159/Domain: acetate-CoA ligase homology <ACL10>
F:13623-13690/Domain: acyl carrier protein homology <ACP10>
F:14213-14676/Domain: acetate-CoA ligase homology <ACL11>
F:14698-14765/Domain: acyl carrier protein homology <ACP11>
F:1060,2558,4045,5537,7034,8094,9589,11086,12158,13654,14729/Binding site: phosphopantetheine
Query Match 6.5%; Score 78.5; DB 2; Length 15281;
Best Local Similarity 24.8%; Pred. No. 2e+03; Matches 55; Indels 73; Gaps 12;
Matches 50; Conservative 24; Mismatches 55; Indels 73; Gaps 12;
QY 37 GAVLLSSFTAMSLYQLAALQADLMRLME--LQSYRG-SATPAAAKLLTPAAPRPHNSS 93
Db 3592 GHVLEVGITGTVLP-----NLGREGGLQSVGLSPSPSATAFVNKAA----- 3634
QY 94 RCHRRRAPPGPEE-----TEQDV-----DLSAPPALRNII-----QDCL-QLIADS 134
Db 3635 -----KSPFGLGDRIRVEVGTATIDRLGDDLHAGLVVNSVAQYFPSPDYLAQLVRD- 3687
QY 135 DPTIRKGYTFVPWLLSPKGNALYSOVLYTDPFAMGHVIR-----KKVHVFGEDELS 189
Db 3688 -----LTKVPGV-----ERIFFGD---MRSHAINRDFLVARAVHALGDKAT 3725
QY 190 LVTLFRFCIONLEEGDEIQLAIP 211
Db 3726 KAEIQREVVVRMESEDELIVDP 3747

Search completed: February 3, 2004, 07:45:39
Job time : 17.4356 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 9.79556 Seconds
(without alignments)
1113.790 Million cell updates/sec

Title: US-09-911-777-2
Perfect score: 1204
Sequence: 1 MDESAKTLPPCLFCSEK.....ENAIQRNGDDTFGALKL 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result #	No.	Score	Match	Query %	ID	Description
1	1103.5	91.7	309	1	T13B_MOUSE	Q9w72 mus musculus
2	622.5	51.7	285	1	T13B_HUMAN	Q9y275 homo sapien
3	151	12.5	241	1	TN13_MOUSE	Q9d777 mus musculus
4	149	12.4	250	1	TN13_HUMAN	O75888 homo sapien
5	83	6.9	410	1	AUP1_MOUSE	P20295 mus musculus
6	81	6.7	449	1	ALGB_PSEAE	P23747 pseudomonas
7	80	6.6	842	1	EP2_SCHPO	O14460 schizosacch
8	79.5	6.6	428	1	HISX_LACPL	P59399 lactobacill
9	79.5	6.6	573	1	SECD_MYCTU	Q50634 mycobacteri
10	79.5	6.6	2167	1	SHK1_RAT	Q9wv48 rattus norv
11	79	6.6	513	1	TI60_HUMAN	Q92993 homo sapien
12	78.5	6.5	498	1	VGLX_PRVRI	P07562 pseudorabie
13	78	6.5	373	1	FLGI_AGRIS	Q44340 agrobacteri
14	77.5	6.4	383	1	VGLZ_HSVK	P32515 equine herp
15	77.5	6.4	454	1	YAP1_HUMAN	P46937 homo sapien
16	77	6.4	732	1	TRPE_AZOB	P50872 azospirillu
17	77	6.4	923	1	HXK3_HUMAN	P52790 homo sapien
18	77	6.4	3023	1	POLG_TVIV	P09814 t genome po
19	76.5	6.4	882	1	DIS1_SCHPO	Q09933 schizosacch
20	76.5	6.4	1755	1	PEPL_MOUSE	Q9r269 mus musculu
21	76	6.3	1403	1	NID2_MOUSE	O88322 mus musculu
22	75.5	6.3	297	1	YPHB_BACSU	P50742 bacillus su
23	75.5	6.3	346	1	TRPA_WAIZE	P42390 zea mays (m
24	75.5	6.3	735	1	IF2C_GUITH	O78489 guillardia
25	75.5	6.3	1210	1	BAT8_HUMAN	Q96kq7 homo sapien
26	75	6.2	430	1	ORC2_CAEEL	Q21037 caenorhabdi
27	74.5	6.2	357	1	MYCM_HUMAN	P12525 homo sapien
28	74.5	6.2	428	1	YQP1_CAEEL	Q09302 caenorhabdi
29	74.5	6.2	448	1	YAP1_CHICK	P46936 gallus gall
30	74	6.1	789	1	PRTP_EBV	P25939 Epstein-Bar
31	74	6.1	797	1	VGLX_HSVB	P28968 equine herp
32	74	6.1	1147	1	SRE1_HUMAN	P36956 homo sapien
33	73.5	6.1	472	1	YFHD_ECOLI	P30135 escherichia

RESULT 1

ID	T13B_MOUSE	STANDARD;	PRT;	309 AA.
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 13B (B cell-activating factor) (BAFF)			
GN	TNFSF13B OR BAFF			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=99288033; PubMed=10359578;			
RA	Schneider P., Mackay F., Steiner V., Hofmann K., Bodmer J.-L.,			
RA	Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,			
RA	Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,			
RA	Tschopp J.;			
RT	"BAFF", a novel ligand of the tumor necrosis factor family, stimulates B cell growth.";			
RL	J. Exp. Med. 189:1747-1756 (1999).			
RN	[2]			
RC	SEQUENCE FROM N.A., AND VARIANT SER-79.			
STRAIN=NZB;				
RA	MEDLINE=21850530; PubMed=11862414;			
RA	Jiang Y., Oheueji M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T.,			
RA	Hirose S.;			
RT	"Polymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family (Baff) and association with the autoimmune phenotype.";			
RL	Immunogenetics 53:810-813 (2001).			
CC	-1- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA. TNFSF13/APRIL binds to the same 2 receptors. Together, they form a 2 ligands - 2 receptors pathway involved in the stimulation of B- and T-cell function and the regulation of humoral immunity. A third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the survival of mature B-cells and the B-cell response.			
CC	-1- SUBUNIT: Homotrimer.			
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.			
CC	-1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.			
CC	-1- SIMILARITY: Belongs to the tumor necrosis factor family.			
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DR	EMBL; AF119383; AAD22475.1; -.			

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DR EMBL; AF352245; AAL83939.1; -.
DR MGD; MGI:134376; Tnfef13b.
DR InterPro; IPR006052; TNF_family.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; FALSE NEG.
DR PROSITE; PS50049; TNF 2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
KW Polymorphism.
FT CHAIN 1 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT CHAIN 127 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT CHAIN 127 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 69 309 EXTRACELLULAR (POTENTIAL).
FT SITE 126 127 CLEAVAGE (BY SIMILARITY).
FT DISULFID 256 269 BY SIMILARITY.
FT CARBOHYD 117 117 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 79 79 N -> S (IN STRAIN NZB).
SQ SEQUENCE 309 AA; 34192 MW; F3DE6056866034B4 CRC64;

Query Match 91.7%; Score 1103.5; DB 1; Length 309;
R Best Local Similarity 74.4%; Pred. No. 2e-96;
R Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;

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DQ 121 GHRNRRAPFGPBETEDVDLSAPPA-----LRNIQDCLQLIADSDTP 180
QY 138 TIRKGTITYFVPWLLSFKEGNAL-----YSQVLTDDIFFANGHVIQRKK 180
DQ 181 TIRKGTITYFVPWLLSFKEGNAL-----YSQVLTDDIFFANGHVIQRKK 240
QY 181 VHVFGDELVLTLFRCION-----LEEGDRIQLAI PRENAQISRGDD 223
DQ 241 VHVFGDELVLTLFRCION-----LEEGDRIQLAI PRENAQISRGDD 300
QY 224 TFFGALKLL 232
DQ 301 TFFGALKLL 309

RESULT 2
T13B HUMAN
ID T13B HUMAN STANDARD; PRT; 285 AA.
AC Q9V275;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13B (TNF- and APOL-
DE related leukocyte expressed ligand 1) (TALL-1) (B lymphocyte
DE stimulator) (BLYS) (B cell-activating factor) (BAFF) (Dendritic cell-
DE derived TNF-like molecule).
GN TNFSF13B OR TALL1 OR BLYS OR BAFF OR ZTNF4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99260341; PubMed=10331498;
RA Shu H.-B., Hu W.-H., Johnson H.;
RT "TALL-1 is a novel member of the TNF family that is down-regulated by

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RT mitogens.";
RN J. Leukoc. Biol. 65:680-683(1999).
RL [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 134-148.
RX MEDLINE=99288033; PubMed=10359578;
RA Schneider P., Mackay P., Steiner V., Hofmann K., Bodmer J.-L.,
RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
RA Valmorli D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
RA Tschopp J.;
RA "BAFF, a novel ligand of the tumor necrosis factor family, stimulates
RT B cell growth.";
RN J. Exp. Med. 189:1747-1756(1999).
RL [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Monocytes, and Neutrophils;
RA MEDLINE=99323343; PubMed=10398604;
RA Moore P.A., Belvedere O., Orr A., Pieri K., Lafleur D.W., Feng P.,
RA Soppet D., Charfers M., Gentz R., Parmelee D., Li Y., Gaiparina O.,
RA Giri J., Roschke V., Nardelli B., Carrell J., Sosnovtseva S.,
RA Greenfield W., Ruben S.M., Olsen H.S., Fikes J., Hilbert D.M.;
RT "Blys: member of the tumor necrosis factor family and B lymphocyte
RT stimulator.";
RL Science 285:260-263(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Farrah T., Gross J., Piddington C., O'Hara P.;
RT "Homo sapiens homolog of tumor necrosis factor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Dendritic cell;
RA Zhang W., Wan T., Yu Y., Cao X.;
RT "A novel dendritic cell-derived TNF-like molecule.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA MEDLINE=22388257; PubMed=12477932;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 1-135 FROM N.A., AND VARIANT THR-105.
RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT "New polymorphisms of human Blys gene.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
RN [9]

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RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 142-285.
 RX MEDLINE=21842897; PubMed=11853672;
 RA Liu Y., Xu L., Opalka N., Kappler J., Shu H.-B., Zhang G.;
 RT "Crystal structure of sTALL-1 reveals a virus-like assembly of TNF
 family ligands";
 RL Cell 108:383-394 (2002).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 136-285.
 RX MEDLINE=21686304; PubMed=11827482;
 RA Karpusas M., Cachero T.G., Qian F., Boriack-Sjodin A., Mullen C.,
 RT Strauch K., Hsu Y.-M., Kallied S.L.;
 RL "Crystal structure of extracellular human BAFF, a TNF family member
 that stimulates B lymphocytes";
 RN J. Mol. Biol. 315:1145-1154 (2002).
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 134-285.
 RX MEDLINE=21912420; PubMed=11862220;
 RA Oren D.A., Li Y., Volovik Y., Morris T.S., Dharla C., Das K.,
 RT Galperina O., Gentz R., Arnold E.;
 RL "Structural basis of BLYS receptor recognition";
 CC Nat. Struct. Biol. 9:288-292 (2002).
 CC -!- FUNCTION: Cytokine that binds to TNFSF13B/TACI and TNFSF17/BCMA.
 CC TNFSF13/APRIL binds to the same 2 receptors. Together, they form a
 CC 2 ligands - 2 receptors pathway involved in the stimulation of B-
 CC and T-cell function and the regulation of humoral immunity. A
 CC third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the
 CC survival of mature B-cells and the B-cell response.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 CC EXTRACELLULAR SOLUBLE FORM.
 CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PERIPHERAL BLOOD
 CC LEUKOCYTES AND IS SPECIFICALLY EXPRESSED IN MONOCYTES AND
 CC MACROPHAGES. ALSO FOUND IN THE SPLEEN, LYMPH NODE, BONE MARROW, T-
 CC CELLS AND DENDRITIC CELLS. A LOWER EXPRESSION SEEN IN PLACENTA,
 CC HEART, LUNG, FETAL LIVER, THYMUS, AND PANCREAS.
 CC -!- INDUCTION: UPREGULATED BY EXPOSURE TO INTERFERON-GAMMA. DOWN-
 CC REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN TREATMENT.
 CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 CC PROTEOLYTIC PROCESSING.
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC -----
 DR EMBL; AF136293; AAD29421.1; -;
 DR EMBL; AF136456; AAD25356.1; -;
 DR EMBL; AF132600; AAD21092.1; -;
 DR EMBL; AF136114; AAF01432.1; -;
 DR EMBL; AF134715; AAF60219.1; -;
 DR EMBL; AB073225; BAB90856.1; -;
 DR EMBL; BC020674; AAH20674.1; -;
 DR PDB; 1KXG; 03-APR-02.
 DR PDB; 1KD7; 12-NOV-02.
 DR PDB; 1JH5; 08-FEB-02.
 DR Genew; HGNC:11929; TNFSF13B.
 DR MIM; 603969; -;
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR006052; TNF_family.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; FALSE_NEG.
 DR PROSITE; PS0049; TNF_2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure;
 KW Polymorphism.
 FT CHAIN 1 285 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

FT CHAIN 134 285 MEMBER 13B, MEMBRANE FORM.
 FT FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT FT MEMBER 13B, SOLUBLE FORM.
 FT FT CYTOPLASMIC (POTENTIAL).
 FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT FT (POTENTIAL).
 FT FT EXTRACELLULAR (POTENTIAL).
 FT FT CLEAVAGE.
 FT FT N-LINKED (GLCNAC. . .).
 FT FT N-LINKED (GLCNAC. . .) (HIGH MANNOSE).
 FT FT A -> T.
 FT FT /FTId=VAR_013483.
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 FT TURN 153 154
 FT STRAND 158 160
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 FT STRAND 163 165
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 FT STRAND 278 283
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 Query Match 51.7%; Score 622.5; DB 1; Length 285;
 Best Local Similarity 48.7%; Pred. No. 3.3e-51;
 Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;
 QY 1 MDESAKTLPPPCLCFCSEKGDMLKV-GYDPTTPROKEGAV-----LSS 43
 DB 1 MDDSTER-EGSLRTSCLKKEEMKLCVSLPRKSPSVRSKDGKLLAATLLALLSC 59
 QY 44 SFTAMSLYQLAALQADLMNLRMELQSVRGSGATPAAA-----KLLTPAA 86
 DB 60 CLTVSVFYQVALQGLDASLAELOCHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
 QY 87 PRPHNSRGHRNRAPFPPETEQVDLSAPPALRNIIQDCLQIADSDTFTIRGTVTF 146
 DB 120 PEGNSGNSNRKRAVQGPET-----VTQDCLQIADSETPTIQGSYTF 165
 QY 147 VPWLLSPKRGNA-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
 DB 166 VPWLLSPKRGSALEEKENKILVETGYFFIYGVQVLYTDKTYAMGHLIQKKVHVFGDELS 225
 QY 190 LVTLPFRICQN-----LEEGDEIQLAIPRENAQISRGDDTFFGALKLL 232
 DB 226 LVTLPFRICQNPPETLPNNNSCYSGIAKLEEGDEIQLAIPRENAQISLDGVTFFGALKLL 285
 RESULT 3
 TN13 MOUSE
 ID TN13 MOUSE STANDARD; PRT; 241 AA.
 AC Q9D777; Q9ERP1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-
 DE inducing ligand) (APRIL).
 GN TNFSF13 OR APRIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RA "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity";
RL Nat. Immunol. 1:252-256(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa K., Izawa M., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Kizawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to
CC TNFRSF17/BCMA. May be implicated in the regulation of tumor cell
CC growth. May be involved in monocyte/macrophage-mediated
CC immunological processes.
CC -!- SUBUNIT: Homotrimer (Potential).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF294825; AAC22534.1; -;
CC EMBL; AK009514; BAB26332.1; -;
CC MGD; MGI:1916833; Tnfef13.
CC GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
CC InterPro; IPR006052; TNF_family.
CC Pfam; PF00229; TNF; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS0049; TNF 2; 1.
CC Cytokine; Immune response; Glycoprotein.
FT PROPEP 1 95
FT CHAIN 96 241
FT
FT BY SIMILARITY.
FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT MEMBER 13.
FT
FT SITE 95 96
FT DISULFID 187 202
FT CARBOHYD 115 115
FT CONFLICT 120 120
SQ SEQUENCE 241 AA; 26889 MW; 4B96D03BDC712A4 CRC64;
Query Match 12.5%; Score 151; DB 1; Length 241;

Best Local Similarity 26.9%; Pred. No. 6.1e-07;
Matches 66; Conservative 24; Mismatches 75; Indels 80; Gaps 9;

Qy 37 GAVLLSSSFYAMSLYQLAQLADLNNRMEQLQSYRGSAATPAAKLLTPAARPHNS----- 92
Db 27 GAVLGAVTCAVALLIQ-----QTEQLSLRRVSRQRSGPSQKQ-----GERPWQSLWEQ 77
Qy 93 -----SRGHRNRRAFPGPETEQVDLSAPPALRNIIQDCLQIADSDTPTIRKG 142
Db 78 SPDVLEAWKCAKSRERRAVLTQKHKHGVHLVPV--NITSK-----ADSDV----- 124
Qy 143 TYTFVPMWLLSPKRGNA-----LYSQVLYTDPIFAMGHVTRQKKVHVFG 185
Db 125 --TEVMQPVLLRRGRGLEAQGDIVRVMDTGILYLSQVLFPHDVTFTMGQVYSRE----- 176
Qy 186 DELSLVTLFRCIQ-----NLEEGDEIQLAIPRENAQISRNGDDTFF 226
Db 177 GQGRRRTLFRCIIRSMPSPPRAYNSCYSAGVFHLHQGDIIIVTKIPRANAKLSLPHGFTFL 236
Qy 227 GALKL 231
Db 237 GFVKL 241

RESULT 4
TN13 HUMAN STANDARD; PRT; 250 AA.
ID O75888; Q96HV6; Q9P1M8; Q9P1M9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-
DE inducing ligand) (APRIL) (TNF- and ABOL-related leukocyte expressed
DE ligand 2) (TALL-2) (TNF-related death ligand-1) (TRDL-1).
GN TNFSF13 OR APRIL OR TALL2 OR ZTNF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=98416181; PubMed=9743536;
RA Hahne M., Kataoka T., Schroeter M., Hofmann K., Imler M.,
RA Bodmer J.-L., Schneider P., Bornand T., Holler N., French L.E.,
RA Sordat B., Rimoldi D., Tschopp J.;
RT "APRIL, a new ligand of the tumor necrosis factor family, stimulates
RT tumor cell growth.";
RL J. Exp. Med. 188:1185-1190(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99260341; PubMed=10331498;
RA Shu H.-B., Hu W.-H., Johnson H.;
RT "TALL-1 is a novel member of the TNF family that is down-regulated by
RT mitogens.";
RL J. Leukoc. Biol. 65:680-683(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Farrah T., Grant F., Haldeman B., Whitmore T., Gross J., O'Hara P.;
RT "Homo sapiens tumor necrosis factor homolog.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
RX MEDLINE=20168636; PubMed=10706119;
RA Kelly K.A., Manos E.J., Jensen G.T., Nadauld L., Jones D.A.;
RT "APRIL/TRDL-1, a tumor necrosis factor-like ligand, stimulates cell
RT death.";
RL Cancer Res. 60:1021-1027(2000).
RN [5]
RP SEQUENCE OF 1-247 FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Heu H., Senaldi G., Theill L.E.,
RA "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.",
RL Nat. Immunol. 1:252-256(2000).
RN [7]
RP PROCESSING BY FURIN, MUTAGENESIS OF ARG-101 AND ARG-104, AND
RP SUBCELLULAR LOCATION.
RX MEDLINE=21486098; PubMed=11571266;
RA Lopez-Fraga M., Fernandez R., Albar J.P., Hahne M.,
RA "Biologically active APRIL is secreted following intracellular
RT processing in the Golgi apparatus by furin convertase.",
RL EMBO Rep. 2:945-951(2001).
CC -!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to
CC TNFRSF17/BCMA. May be implicated in the regulation of tumor cell
CC growth. May be involved in monocyte/macrophage-mediated
CC immunological processes.
CC -!- SUBUNIT: Homotrimer (Potential).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=Alpha;
CC IsoId=O75888-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=O75888-2; Sequence=VSP_006450;
CC Name=Gamma;
CC IsoId=O75888-3; Sequence=VSP_006451;
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN TRANSFORMED CELL
CC LINES, CANCERS OF COLON, THYROID, LYMPHOID TISSUES AND
CC SPECIFICALLY EXPRESSED IN MONOCYTES AND MACROPHAGES.
CC -!- INDUCTION: DOWN-REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN
CC TREATMENT.
CC -!- PTM: The precursor is cleaved by furin.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF046888; AAC61312.1; -
CC EMBL; AF136294; AAD29422.1; -
CC EMBL; AF184972; AAF01321.1; -
CC EMBL; AF114011; AAF59828.1; -
CC EMBL; AF114012; AAF59829.1; -
CC EMBL; AF114013; AAF59830.1; -
CC EMBL; BC008042; AAH08042.1; -

DR Genew; HGNC:11928; TNFSF13.
DR MIM; 604472; -
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006052; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS00049; TNF 2; 1.
KW Cytokine; Immune response; Glycoprotein;
KW Alternative splicing.
FT PROPEP 1 104
FT CHAIN 105 250
FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT MEMBER 13.
FT CLEAVAGE (BY FURIN).
FT POTENTIAL.
FT N-LINKED (GLCNAC..) (POTENTIAL).
FT KOHSLVHLVFNATSKD -> N (in isoform Beta).
FT /FTID=VSP_006450.
FT Missing (in isoform Gamma).
FT /FTID=VSP_006451.
FT EKRR->AKRA; ABOLISHES PROTEOLYTIC
FT PROCESSING.
FT N -> S (IN REF. 5).
FT CONFLICT 96 247
FT CONFLICT 247 247
SQ SEQUENCE 250 AA; 27433 MW; AEA6B9457F6E298 CRC64;
Query Match 12.4%; Score 149; DB 1; Length 250;
Best Local Similarity 25.9%; Pred. No. 9.9e-07;
Matches 58; Conservative 27; Mismatches 73; Indels 66; Gaps 7;
QY 53 LAALQADLMRLMELQSVRGSGATPAAXALLTPAAPRHNS-----RGHRNRAPP 103
DB 48 LLTQTELOSLRREVSRLQGTGGPQNGEGVWQSLPQSSDALAEWNGERSRRRAVL 107
QY 104 GPEETEQDVLSAPPALRNIIQDCLLIADSDTPTIRKGTVTFFVWLLSFKRGNA----- 158
DB 108 TQKQKQSHLVHLV-INATSKD-----DSDV-----TEVMQPALRRGRGLQAQG 152
QY 159 -----LYSQVLYTDPFAMGHVIOQRKVVHFGDELVLTLPRCIO----- 198
DB 153 YGVRIQDAGVYLLYVQLFDVFTFMGVVSRE-----GQGRQETLFRICRSMPSHPDR 206
QY 199 -----NLEGGDIQALIPRENAQISRGDDTFFGALKL 231
DB 207 AYNSCYSAGVPHLHQSDILSVIIPARAKLNLSPHGTFLGFVKL 250
RESULT 5
AUP1_MOUSE
ID AUP1_MOUSE STANDARD; PRT; 410 AA.
AC P70295;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ancient ubiquitous protein 1 precursor.
GN AUP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=96411699; PubMed=8812468;
RA Jang W., Weber J.S., Bashir R., Bushby K., Meisler M.H.;
RT "Aup1, a novel gene on mouse chromosome 6 and human chromosome 2p13.",
RL Genomics 36:366-368(1996).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: BELONGS TO THE AUP1 FAMILY.
CC -----
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EMBL; U41736; AAC52839.1; -;
MGD; MGI:107789; Aupl.
InterPro; IPR002123; Acyltransferase.
InterPro; IPR003892; CUB.
Pfam; PF02845; CUB; 1.
SMART; SM00546; CUB; 1.
SMART; SM00563; PLS; 1.
Signal.
CHAIN 1 37 POTENTIAL.
CHAIN 38 410 ANCIENT UBQUITOUS PROTEIN 1.
SEQUENCE 410 AA; 46121 MW; E7D070CEB296B5B CRC64;

Query Match 6.9%; Score 83; DB 1; Length 410;
Best Local Similarity 22.1%; Pred. No. 3.1;
Matches 44; Conservative 20; Mismatches 77; Indels 58; Gaps 7;

4 SAKTLPPCLPCSCSGEDMKVG-----YDTPPKKEGAV----- 39
148 STRLPPTLLLPPEEATNGREGLRFSSWPFISQDVVQPLTLQVQRLVSVTVSDASWV 207
40 --LLSSSTANSLYOLALQADLMNLMELQSYRGSSATPAAK-----LLTPAAPRH 90
208 SELLWSLFPVFTYQVRLHPTRQLGSEEFALRVQOLVAKELGQIGTRITPADKAH 267
91 NSSRGHNR-----APGPETEQQVDLSA-----PPALRNIIQ-----DCLQ 129
268 MKQRHPRLRPOSVOSSPSPSPSDVLTTLAHRVKEVLPVPLNVIQRLARTGCV 327
130 LIADSDTPTIRKGYTFVP 148
328 LTTN-----LLEGAVAFNP 342

RESULT 6

ALGB_PSEAE STANDARD; PRT; 449 AA.
AC P23747;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alginate biosynthesis transcriptional regulatory protein algb.
GN ALGB OR PA5483.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate FRD;
RX MEDLINE=91139582; PubMed=1899859;
RA Wozniak D.J., Ohman D.E.;
RT "Pseudomonas aeruginosa Algb, a two-component response regulator of the NtrC family, is required for algd transcription.";
RL J. Bacteriol. 173:1406-1413 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92149314; PubMed=1738315;
RA Goldberg J.B., Danke T.;
RT "Pseudomonas aeruginosa Algb, which modulates the expression of alginates, is a member of the NtrC subclass of prokaryotic regulators.";
RL Mol. Microbiol. 6:59-66 (1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brady L.L., Coulter S.N., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
RL Nature 406:959-964 (2000).
CC -!- FUNCTION: POSITIVE REGULATOR OF ALGINATE BIOSYNTHETIC GENE (ALGD).
CC -!- SIMILARITY: Contains 1 response regulatory domain.
CC -!- SIMILARITY: Contains 1 sigma-54 factor interaction ATP-binding domain.

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EMBL; M62902; AAA25700.1; -;
EMBL; M82823; -; NOT ANNOTATED CDS.
EMBL; AE004961; AAG08688.1; -;
PIR; A38449; A38449.

HSSP; P41789; 1NTR.

InterPro; IPR003593; AAA ATPase.

InterPro; IPR002197; HTH_Pis

InterPro; IPR001789; Response_reg.

InterPro; IPR002078; Sig54_interact.

Pfam; PF02954; HTH_8; 1.

Pfam; PF00072; response_reg; 1.

Pfam; PF00158; Sigma54_activat; 1.

ProDom; PD000039; Response_reg; 1.

SMART; SM00382; AAA; 1.

SMART; SM00448; REC; 1.

TIGRFAMs; TIGR01199; HTH_fis; 1.

PROSITE; PS01110; RESPONSE REGULATORY; 1.

PROSITE; PS00675; SIGMA54_INTERACT_1; 1.

PROSITE; PS00676; SIGMA54_INTERACT_2; 1.

PROSITE; PS00688; SIGMA54_INTERACT_3; 1.

PROSITE; PS0045; SIGMA54_INTERACT_4; 1.

Sensory transduction; Phosphorylation; Transcription regulation;

DNA-binding; Activator; ATP-binding; Alginates biosynthesis;

Complete proteome.

DOMAIN 10 124 RESPONSE REGULATORY.

MOD_RES 59 59 PHOSPHORYLATION (BY SIMILARITY).

DOMAIN 147 376 SIGMA-54 FACTOR INTERACTION (POTENTIAL).

NP_BIND 175 182 ATP (POTENTIAL).

NP_BIND 238 247 ATP (POTENTIAL).

DNABIND 426 445 H-T-H MOTIF (BY SIMILARITY).

SEQUENCE 449 AA; 49323 MW; E6452B88457CBC17 CRC64;

Query Match 6.7%; Score 81; DB 1; Length 449;

Best Local Similarity 25.7%; Pred. No. 5.3;

Matches 37; Conservative 18; Mismatches 63; Indels 26; Gaps 6;

Qy 7 TLPPCLPCSCSGEDMKVGYPIT-----PQEEGAVLLSSSTAMSLYQALAL 56
Db 254 TLQPKLLRFIQDK-EYERVG-DPVTTRADVRILATNRDLGAMVAQGFREDLLRLNVI 311
Qy 57 QADLMNLMELQSYRGSSATPAAKLTP-AAPRPHNSRGHNRRAFPGPETEQQVDLS 115
Db 312 VLNLPPLLEAEADILGLAEFLARFVKDYGRGPFSEAEAREMKQYFPGVNVRE----- 366
Qy 116 APPALRNIIQD-----CQLIADSD 135
Db 367 ----LRNVIERASIIICQELVDVD 386

RESULT 7

EF2_SCHPO STANDARD; PRT; 842 AA.
ID EF2_SCHPO

AC 014460; Q9USG7; Q9US29; Q9UT64;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor 2 (EF-2).
 GN (EFT1 OR SPCP1B10.07) AND (EFT2 OR SPAC513.01C OR SPAPYU71.04C).
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=97254480; PubMed=9098980;
 RA Mita K., Morimoto M., Ito K., Sugaya K., Ebihara K., Hongo E.,
 RA Higashi T., Hirayama Y., Nakamura Y.,
 RA "Comprehensive cloning of Schizosaccharomycetes pombe genes encoding
 RT translation elongation factors.";
 RL Gene 187:259-266(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (EFT1 AND EFT2).
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornaby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leacher S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell J.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakowski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe.";
 RL Nature 415:871-880(2002).
 CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
 CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
 CC RIBOSOME (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
 CC EF-G/EF-2 SUBFAMILY.
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 CC
 CC EMBL; D83976; BA23591.1;
 CC EMBL; D83975; BA23590.1;
 CC EMBL; AL121859; CAB58373.1;
 CC EMBL; AL122032; CAB58724.1;
 CC EMBL; AL109734; CAB52147.1;
 CC FIC; T41697; T41697.
 CC GeneDB_Spombe; SPAC513.01c;
 CC GeneDB_Spombe; SPCP1B10.07;

DR InterPro; IPR000795; EF_GTPbind.
 DR InterPro; IPR000640; EFG_C.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF00679; EFG_C; 1.
 DR Pfam; PF03764; EFG_IV; 1.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 DR PRINTS; PR00315; ELONGATNFC.
 DR TIGRFAMs; TIGR00231; small_GTP; 1.
 DR PROSITE; PS00301; EFATOR_GTP; 1.
 KW Elongation factor; Protein biosynthesis; GTP-binding.
 FT NP_BIND 26 33 GTP (BY SIMILARITY).
 FT NP_BIND 104 108 GTP (BY SIMILARITY).
 FT NP_BIND 158 161 GTP (BY SIMILARITY).
 FT MOD_RES 699 699 DIPHTHAMIDE (BY SIMILARITY).
 FT CONFLICT 821 823 EAR -> DVG (IN REF. 1).
 SQ SEQUENCE 842 AA; 93230 MW; A544C5C454BC55C7 CRC64;
 Query Match 6.6%; Score 80; DB 1; Length 842;
 Best Local Similarity 20.2%; Pred. No. 15;
 Matches 53; Conservative 28; Mismatches 76; Indels 106; Gaps 12;
 QY 11 PC-ICFCSEKEDMKVGYDPTPOKEEGAVLLSSFTAMSLYQLAALQADLNLRLQ- 68
 DB 516 PCVLCTTSSEGEHIVAG-----AGELHLEIC-----LKDLOEDHAGIPLKISP 558
 QY 69 ---SVRGATPAAKLLTPAAPRHNS-----SRGHENRR----- 100
 DB 559 PWSYRESVSEPSMTALSKSPKHNRIFTAEPMSELSVAIETGHVNPDDDFKVRARI 618
 QY 101 -----APFGPEETEED--VDLSAPPALRNIIQD----- 126
 DB 619 MADEFGWDVTARKIWC-FGDTTCANVVVDQTKAVYLNIKSVVAAFAWASKEGPMF 677
 QY 127 -----CLQIADSDTPIRKGTFTFVFWLLSKFGNALYSQVLYTDPF----- 170
 DB 678 EENLRSCRFNLDVVLHAD--AIHGGGQIITARRVVVYSTLLASPIQEPVFLVEIQV 735
 QY 171 ---AMG---HVIQRKVVHVGDE 187
 DB 736 SENAMGGIYSVLNKKRGHVFSEE 758
 RESULT 8
 HISX_LACPL STANDARD; PRT; 428 AA.
 ID HISX_LACPL AC P59399;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Histidinol dehydrogenase (EC 1.1.1.23) (HDH).
 GN HISD OR LP 2559.
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 8826 / WCFS1;
 RX MEDLINE=22480296; PubMed=12566566;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hofer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Siezen R.J.;
 RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 CC -!- FUNCTION: Catalyzes the sequential NAD-dependent oxidations of L-
 CC histidinol to L-histidinolaldehyde and then to L-histidine (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: L-histidinol + 2 NAD(+) + H(2)O = L-histidine

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CC      + 2 NADH.
CC      -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC      -!- PATHWAY: Histidine biosynthesis; ninth (last) step.
CC      -!- SIMILARITY: Belongs to the histidinol dehydrogenase family.
CC
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CC
CC      EMBL; AL935259; CAD64837.1; -.
DR      HAMAP; MF 01024; -.
DR      PROSITE; PS00611; HISOL_DEHYDROGENASE; FALSE NEG.
KW      Histidine biosynthesis; Oxidoreductase; NAD; Metal-binding; Zinc;
KW      Complete proteome.
FT      ACT SITE 322 322 BY SIMILARITY.
FT      ACT SITE 323 323 BY SIMILARITY.
FT      METAL 254 254 ZINC (BY SIMILARITY).
FT      METAL 257 257 ZINC (BY SIMILARITY).
FT      METAL 356 356 ZINC (BY SIMILARITY).
FT      METAL 415 415 ZINC (BY SIMILARITY).
SQ      SEQUENCE 428 AA; 45985 MW; 9DE9DDE6D8487D2C CRC64;
Query Match 6.6%; Score 79.5; DB 1; Length 428;
Best Local Similarity 18.8%; Pred. No. 6.9;
Matches 43; Conservative 35; Mismatches 84; Indels 67; Gaps 8;
QY      30 ITPQKEG---AVLLSSSTFAM-SLYQLAALQADLMNLMELQSYRGSATPAAKLLTPA 85
DB      155 VTPQVDGINPAVLAAXIAGVDAYIQVGGQA-----IAALAYGTESIPAVDKIIGPG 208
QY      86 APRPHNSRGHNRAP-----PGPEE-----TEQVDLSAPP 118
DB      209 -----NIFVATAKQVQGVQVADMVAGPSEIGILADDSADPQLAALLSQAEHRRARP 263
QY      119 ALRNIQCLQIADSDPTTRKGYTFVFWLLSPKRGNALYSQVLYTDPFAMGHVQIR 178
DB      264 ILITDSADLAQVSNVTSQK-----VLPREAIATDANVEKGFIAV 306
QY      179 KKHVFGDELIVTLFRCLQNLLEGEIQLAIPRENAQISRGDDTFFG 227
DB      307 AKIEREMFDMNTVA-----PEHLEVQLKNPTQVLYLNKRGVSVFLG 347
RESULT 9
SECD MYCTU
ID SECD MYCTU STANDARD; PRT; 573 AA.
AC Q50634;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein-export membrane protein secd.
GN SECD OR RV2587C OR MT2664 OR MTCY227.14.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=982955987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skellon S., Squares S., Squares R.,
RA Sultston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the

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RT      complete genome sequence."
RL      Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey B.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT      "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT      laboratory strains."
RL      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: INVOLVED IN PROTEIN EXPORT.
CC      -!- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLLOCATION APPARATUS
CC      WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECH
CC      (BY SIMILARITY).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC      -!- SIMILARITY: BELONGS TO THE SECD/SECF FAMILY. SECD FAMILY.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; Z77724; CAB01256.1; -.
DR      EMBL; AE007100; AAK46977.1; ALT_INIT.
DR      PIR; B70726; B70726.
DR      TIGR; MT2664; -.
DR      TubercuList; RV2587C; -.
DR      InterPro; IPR005791; SecD.
DR      InterPro; IPR003335; SecD_SecF.
DR      Pfam; PF02355; SecD_SecF; 1.
DR      TIGRFAMs; TIGR00916; 2A0604s01; 1.
DR      TIGRFAMs; TIGR01129; secd; 1.
KW      Protein transport; Translocation; Transmembrane; Membrane;
KW      Complete proteome.
FT      TRANSMEM 13 33 POTENTIAL.
FT      TRANSMEM 385 405 POTENTIAL.
FT      TRANSMEM 410 430 POTENTIAL.
FT      TRANSMEM 441 461 POTENTIAL.
FT      TRANSMEM 489 509 POTENTIAL.
FT      TRANSMEM 514 534 POTENTIAL.
SQ      SEQUENCE 573 AA; 60267 MW; 5A8F42E2C0389CE2 CRC64;
Query Match 6.6%; Score 79.5; DB 1; Length 573;
Best Local Similarity 22.3%; Pred. No. 10;
Matches 46; Conservative 23; Mismatches 80; Indels 57; Gaps 9;
QY      74 ATPAAKLLTPAAPRPHNSRGHNRAPFCPEETEQQVDLSAPPA----- 119
DB      149 AAPPPAQSGAPAPQPGAPRPYQDPFA-PSPNPTSPASPPPAEAPATDPKDLAER 207
QY      120 -----LRNIQDCLQI-----ADSDTP-----TIRKGYTFVFWPL 150
DB      208 IAQSKKLQSTNQVQWVALQFOATRCESDILLAGNDPKLPVTCSDTKHTAYLLAPSI 267
QY      151 LSPFKRGNALYSQVLYTDPFAMGHVQIRK-----KVHFGD-----ELSLVTLFRCLQNL 202
DB      268 IS---GDIQIATSGMDQ-RGIGYVVDLQFKGPAANIWADYTAAHIGTQTATLDSQVVS 323
QY      203 GDEIQLAIPRENAQISRGDDTFFGA 228
DB      324 APQIQEAIPGRTQIS-GGDPFFTA 348
RESULT 10
SHKL RAT
ID SHKL RAT STANDARD; PRT; 2167 AA.
AC Q9WV48; Q9QZ28; Q9WU13; Q9WUE8;

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DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE SH3 and multiple ankyrin repeat domains protein 1 (Shank1) (GKAP/SAPAP
 DE interacting protein) (SPANK-1) (Synamon) (Somatostatin receptor
 DE interacting protein) (SSTR interacting protein) (SSTRIP).
 GN SHANK1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3), AND INTERACTION WITH DLGAP1 AND
 RP DLG4.
 RC TISSUE=Brain;
 RX MEDLINE=99419021; PubMed=10488079;
 RA Yao I., Hata Y., Hirao K., Deguchi M., Ide N., Takeuchi M., Takai Y.;
 RT "Synamon, a novel neuronal protein interacting with synapse-associated
 RT protein 90/postsynaptic density-95-associated protein.";
 RT J. Biol. Chem. 274:27463-27466(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 4), AND INTERACTION WITH DLGAP1.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=99360850; PubMed=10433268;
 RA Naisbitt S., Kim E., Tu J.C., Xiao B., Sala C., Valtschanoff J.,
 RT Weinberg R.J., Worley P.F., Sheng M.;
 RT "Shank, a novel family of postsynaptic density proteins that binds to
 RT the NMDA receptor/PSD-95/GKAP complex and cortactin.";
 RT Neuron 23:569-582(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=20549637; PubMed=10958799;
 RA Tobaben S., Suedhof T.C., Stahl B.;
 RT "The G protein-coupled receptor C11 interacts directly with proteins
 RT of the Shank family.";
 RT J. Biol. Chem. 275:36204-36210(2000).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5), AND
 RP DEVELOPMENTAL STAGE.
 RC TISSUE=Brain;
 RX MEDLINE=99436166; PubMed=10506216;
 RA Lim S., Naisbitt S., Yoon J., Hwang J.I., Suh P.G., Sheng M., Kim E.;
 RT "Characterization of the Shank family of synaptic proteins. Multiple
 RT genes, alternative splicing, and differential expression in brain and
 RT development.";
 RT J. Biol. Chem. 274:29510-29518(1999).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=Brain;
 RX MEDLINE=20020275; PubMed=10551867;
 RA Zitzer H., Hoeneck H.-H., Baechner D., Richter D., Kreienkamp H.-J.;
 RT "Somatostatin receptor interacting protein defines a novel family of
 RT multidomain proteins present in human and rodent brain.";
 RT J. Biol. Chem. 274:32997-33001(1999).
 RN [6]
 RP INTERACTION WITH HOMER-1, AND SUBCELLULAR LOCATION.
 RX MEDLINE=99360651; PubMed=10433269;
 RA Tu J.C., Xiao B., Naisbitt S., Yuan J.P., Petralia R.S., Brakeman P.,
 RA Doan A., Aakalu V.K., Lanahan A.A., Sheng M., Worley P.F.;
 RT "Coupling of mGluR/Homer and PSD-95 complexes by the Shank family of
 RT postsynaptic density proteins.";
 RT Neuron 23:583-592(1999).
 RN [7]
 RP INTERACTION WITH SPTAN1.
 RX MEDLINE=21523912; PubMed=11509555;
 RA Bockers T.M., Maneva M.G., Kreutz M.R., Bockmann J., Weise C.,
 RA Buck F., Richter D., Gundelfinger E.D., Kreienkamp H.-J.;
 RT "Synaptic scaffolding proteins in rat brain. Ankyrin repeats of the
 RT multidomain Shank protein family interact with the cytoskeletal
 RT protein alpha-fodrin.";
 RT J. Biol. Chem. 276:40104-40112(2001).
 RN [8]

RP FUNCTION.
 RX MEDLINE=21389514; PubMed=11498055;
 RA Sala C., Piech V., Wilson N.R., Passafium M., Liu G., Sheng M.;
 RT "Regulation of dendritic spine morphology and synaptic function by
 RT Shank and Homer.";
 RL Neuron 31:115-130(2001).
 RN [9]
 RP REVIEW.
 RX MEDLINE=20267867; PubMed=10806096;
 RA Sheng M., Kim E.;
 RT "The Shank family of scaffold proteins.";
 RL J. Cell Sci. 113:1851-1856(2000).
 CC -!- FUNCTION: Seems to be an adapter protein in the postsynaptic
 CC density (PSD) of excitatory synapses that interconnects receptors
 CC of the postsynaptic membrane including NMDA-type and metabotropic
 CC glutamate receptors, and the actin-based cytoskeleton. May play a
 CC role in the structural and functional organization of the
 CC dendritic spine and synaptic junction. Overexpression promotes
 CC maturation of dendritic spines and the enlargement of spine heads
 CC via its ability to recruit Homer to postsynaptic sites, and
 CC enhances presynaptic function.
 CC -!- SUBUNIT: May homomultimerize via its SAM domain. Interacts with
 CC SPTAN1, Homer-1 and DLGAP1/GKAP. Is part of a complex with
 CC DLG4/PSD-95 and DLGAP1/GKAP. Interacts with SSTR2 C-terminus via
 CC the PDZ domain (by similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; postsynaptic density of
 CC neuronal cells. Colocalizes with alpha-latrotoxin receptor 1.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing. Named isoforms=5;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=Q9WV48-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9WV48-2; Sequence=VSP_006072, VSP_006073;
 CC Name=3;
 CC IsoId=Q9WV48-3; Sequence=VSP_006074;
 CC Name=4; Synonyms=A;
 CC IsoId=Q9WV48-4; Sequence=VSP_006075;
 CC Name=5;
 CC IsoId=Q9WV48-5; Sequence=VSP_006076, VSP_006077;
 CC -!- TISSUE SPECIFICITY: Expressed only in brain (neuropil of cortex,
 CC CA1 region hippocampus and molecular layer of cerebellum).
 CC -!- DEVELOPMENTAL STAGE: Expression increases from low levels at birth
 CC to high levels at 3-4 weeks before dropping slightly in adulthood.
 CC Expressed in the cortex and the molecular layer of the cerebellum
 CC at postnatal day 7. Isoform 2 expression does not change during
 CC development of both cortex and cerebellum. Isoform 4 expression
 CC decreases significantly during development of cortex but not
 CC cerebellum.
 CC -!- SIMILARITY: BELONGS TO THE SHANK FAMILY.
 CC -!- SIMILARITY: Contains 7 ANK repeats.
 CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
 CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
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 CC -----
 CC EMBL; AF102855; AAD04569.2; -;
 CC EMBL; AF131951; AAD2947.1; ALT_INIT.
 CC EMBL; AF159046; AAD42975.1; -;
 CC EMBL; AF141904; AAF02498.1; ALT_INIT.
 CC HSSP; P00519; IABL.
 CC InterPro; IPR002110; ANK.
 CC InterPro; IPR001478; PDZ.
 CC InterPro; IPR001660; SAM.
 CC InterPro; IPR001452; SH3.
 CC Pfam; PF00023; ank; 7.

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DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF00018; SH3; 1.
DR ProDom; PRO00066; SH3; 1.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00454; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00088; ANK_REPEAT; 3.
DR PROSITE; PS00297; ANK_REPEAT; 1.
DR PROSITE; PS0106; PDZ; 1.
DR PROSITE; PS00028; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW ANK repeat; SH3 domain; Repeat; Alternative splicing.
FT REPEAT 195 210
FT REPEAT 212 245
FT REPEAT 246 278
FT REPEAT 279 312
FT REPEAT 313 345
FT REPEAT 346 378
FT REPEAT 379 395
FT DOMAIN 554 613
FT DOMAIN 663 757
FT DOMAIN 2104 2167
FT DOMAIN 929 932
FT DOMAIN 1010 1015
FT DOMAIN 1022 1027
FT DOMAIN 1194 1199
FT DOMAIN 1850 1860
FT VARSPLIC 1 613
FT VARSPLIC 615 654
FT VARSPLIC 646 654
FT VARSPLIC 797 804
FT VARSPLIC 1930 1943
FT VARSPLIC 1944 2167
FT CONFLICT 1141 1141
FT CONFLICT 1174 1174
FT CONFLICT 1246 1246
FT CONFLICT 1323 1323
FT CONFLICT 1331 1331
FT CONFLICT 1726 1726
FT CONFLICT 2167 AA; 226333 MW; 3F479BSA7B18BA86 CRC64;
SQ SEQUENCE 2167 AA; 226333 MW; 3F479BSA7B18BA86 CRC64;

Query Match 6.6%; Score 79.5; DB 1; Length 2167;
Best Local Similarity 24.8%; Pred. No. 59;
Matches 40; Conservative 24; Mismatches 50; Indels 47; Gaps 8;

QY 1 MDES-----AKTLPPLCLFCSE-----KCEDMKVGVDPTPK-----EEGAVLSS 43
DB 762 MDEAVHKASQQAQKRLPPPAISLRKSMTSELEEM-----VSPWKKXIEYEQPAAVPS 815
QY 44 SFTMSLYLQALQADLMNLMELQSYRGSATPAAAKU-----LTPAAPRPHN 91
DB 816 MEKKTVVQMALNKLDI-LAAQQTISASESPGGLASLGKHPKGPFPATESFDPHH 874
QY 92 SSRGHRNRAP--PGP-----EETEQQVDLSAPPALR 121
DB 875 RQSPQSVDRPSFLPPGPGMLRQKSGAEDDRPYLAPPAMK 915

RESULT 11
T160 HUMAN
ID T160 HUMAN STANDARD; PRT; 513 AA.
AC Q92993; Q95624; Q13430; Q9BNK7;
```


RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland B., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RA "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurrello B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmli K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lapas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RA "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
CC -!- FUNCTION: ASSEMBLES AROUND THE ROD TO FORM THE L-RING AND PROBABLY
CC PROTECTS THE MOTOR/BASAL BODY FROM SHEARING FORCES DURING
CC ROTATION.
CC -!- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE
CC FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)
CC MOUNTED ON A CENTRAL ROD (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the flgI family.
CC
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CC
CC EMBL; U39941; AAB68970.1; -;
CC EMBL; U51165; AAB71792.1; -;
CC EMBL; AE009024; AAL41567.1; -;
CC EMBL; AE007990; AAK86362.1; -;
CC PIR; A97426; A97426.
CC HAMAP; MF_00416; -; 1.
CC InterPro; IPR001782; Flag_FlgI.
DR Pfam; PF02119; FlgI; 1.
DR PRINTS; PRO1010; FLGPRINGFLGI.
KW Flagella; Periplasmic; Signal; Complete proteome.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 373 FLAGELLAR P-RING PROTEIN.
SQ SEQUENCE 373 AA; 38967 MW; 2BCBC695971CF8A5 CRC64;
Query Match 6.5%; Score 78; DB 1; Length 373;
Best Local Similarity 24.7%; Pred. No. 8;
Matches 56; Conservative 31; Mismatches 84; Indels 56; Gaps 11;
QY 18 EKGEDEMK-VGYDPTTPQKEGAVLLSSFTAMSLYQLAALQADLANLRLWELQSVRGSATP 76
DB 38 QAGRNDQLIGYGLVGLQGTGSLRSPPTES-----MRAMLQNLGITTTGGGOSNAK 91
QY 77 AAALKLTTPAAPRHNSRGRNRRAFPQPEETEQQVDLSA-----PALR--NIIDCL--- 128
DB 92 IAAVNVNTANLP-PF-----ASPG---SRVDVTYSSLDGATSLAGNLIWTSLSGA 137
QY 129 --QLIADSDTPTIRKGTTFVFWLLSFKRGNALYSQVLYTDPIFAMGHVIOQRKKVHVFGD 186

Db 138 DQIYAVAOQALIVNG-----FSAQGDAAITLQGVTTTSARVPNGAIIERELPSKPKD 189
QY 187 ELSLVTLFR-----CIQNLBEGDEIQLAIPRENAQIS 218
Db 190 SVNVLQLRPDPFSTAVRVADVNVAFARVGDPI--AEPRDSQIEA 234
RESULT 14
VGLZ_HSVKEK STANDARD; PRT; 383 AA.
AC P32515; 1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Glycoprotein precursor.
GN US4.
OS Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92263758; PubMed=13116673;
RA Colle C.F. III, Flowers C.C., O'Callaghan D.J.;
RT "Open reading frames encoding a protein kinase, homolog of
RT glycoprotein gX of pseudorabies virus, and a novel glycoprotein map
RT within the unique short segment of equine herpesvirus type 1.";
RL Virology 188:545-557(1992).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; M87497; AAA46072.1; -;
DR PIR; C42538; VGBEKG.
KW Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 383 GLYCOPROTEIN.
FT DOMAIN 23 75 SER/THR-RICH.
FT TRANSMEM 354 371 POTENTIAL.
FT CARBOHYD 48 48 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 383 AA; 41027 MW; B390611414131C2B CRC64;
Query Match 6.4%; Score 77.5; DB 1; Length 383;
Best Local Similarity 20.9%; Pred. No. 9.2;
Matches 43; Conservative 24; Mismatches 78; Indels 61; Gaps 8;
QY 73 SATPAAAKLTTPAAPRHNSRGRNR-----RAFPQPEETEQQVD 113
DB 62 SSPPTSTHTSSPSTANAKQKHGRAGRGRRGSGQSGHTTTPHDLRTPSPDYDD-D 120
QY 114 LSAPALRNIIQDCLLIADSDTPTIRKGTTF-----VPMWL----- 151
DB 121 TNHENGNNISLIVPQL--PPDRPIELGVATLRKFNMEASCTVETNSDLAIFWKIGKPS 178
QY 152 --SPKRGNALYSQVLYTDPIFAMGHVIOQRKKVHVFGDELSLVTLFRCLQNLBEGDEIQL- 208
DB 179 VDAFNRGTTHRLMRNGVPVVALVTLRVPMLNVI--PLTKITCAACPTNLVAGDGVLDN 236
QY 209 -----AIP-----RENAQISRNGD 222
DB 237 SCTTKSTTTPCGQOQRTHTPFPSAKGD 262
RESULT 15
YAPI_HUMAN STANDARD; PRT; 454 AA.
ID YAPI_HUMAN
AC P46937;

Search completed: February 3, 2004, 07:44:16
Job time : 11.7956 secs

```
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 65 kDa Yes-associated protein (YAP65).
GN YAP1 OR YAP65
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95301570; PubMed=7782338;
RA Sudol M., Bork P., Einbond A., Kastury K., Druck T., Negrini M.,
RA Huebner K., Lehman D.;
RT "Characterization of the mammalian YAP (Yes-associated protein) gene
RT and its role in defining a novel protein module, the WW domain.";
RL J. Biol. Chem. 270:14733-14741(1995).
RN [2]
RP INTERACTION WITH WBP1 AND WBP2.
RX MEDLINE=97347517; PubMed=9202023;
RA Chen H.I., Einbond A., Kwak S.-J., Linn H., Koepf E., Peterson S.,
RA Kelly J.W., Sudol M.;
RT "Characterization of the WW domain of human Yes-associated protein and
RT its polyproline containing ligands.";
RL J. Biol. Chem. 272:17070-17077(1997).
CC -!- SUBUNIT: Binds to the SH3 domain of the YES kinase. Binds to WBP1
CC and WBP2.
CC -!- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 WW domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X80507; CAA56672.1; -
DR FIR; A56954; A56954.
DR PDB; 1JMQ; 21-DEC-01.
DR PDB; 1K9Q; 28-DEC-01.
DR PDB; 1K9R; 28-DEC-01.
DR Genew; HGNC:16262; YAP1.
DR MIM; 606608.
DR GO; GO:0005515; F:protein binding activity; TAS.
DR InterPro; IPR005153; MbCh.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR Pfam; PF00397; WW; 1.
DR SMART; SM00456; WW; 1.
DR PROSITE; PS01159; WW_DOMAIN_1; 1.
DR PROSITE; PS00200; WW_DOMAIN_2; 1.
KW Phosphorylation; 3D-Structure.
FT DOMAIN 171 204 WW.
SQ SEQUENCE 454 AA; 48755 NW; 87CB840D3393BFC0 CRC64;

Query Match 6.4%; Score 77.5; DB 1; Length 454;
Best Local Similarity 20.8%; Pred. No. 12;
Matches 30; Conservative 16; Mismatches 61; Indels 37; Gaps 3;

QY 1 MDESAKTLPPPCLCFCSEKEDMKVGYDPTTPQKEGAVLLSSFTAMSLYQLAALQADL 60
Db 235 ISQSAPVKQPP-----PLAQSPQGGVGGSGNSNQOQMRLOQLEK 277
QY 61 MNLRLMELQSYRGSAIPAAKLTTPAAPRHNSRGRHNRRAFPGPETEEDVDLSAPPAL 120
Db 278 ERLRLKQQLLRQVRPELAL-----RSQLP---TLEQDGGTGNPVSS 317
QY 121 RNIIQDCLQLIADSDTPTIRKGY 144
Db 318 PGMQSGLRTMTTNSDPLNSGTY 341
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 30.9333 Seconds
(without alignments)
1935.395 Million cell updates/sec

Title: US-09-911-777-2
Perfect score: 1204
Sequence: 1 MDESARTLPPCLCFCSERK.....ENAIISRNDDTFFGALKLL 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	909	75.5	258	11 Q8BZM8	Q8bzm8 mus musculus
2	674.5	56.0	199	11 Q8BWP2	Q8bwp2 mus musculus
3	673.5	55.9	194	11 Q8BVA3	Q8bva3 mus musculus
4	541.5	45.0	208	4 Q8IZI6	Q8izi6 homo sapien
5	522	43.4	174	4 Q8IZI5	Q8izi5 homo sapien
6	490	40.7	158	4 Q8IZI4	Q8izi4 homo sapien
7	430.5	35.8	288	13 Q8JHJ4	Q8jhj4 gallus gall
8	152	12.6	410	11 Q8BXS2	Q8bxs2 mus musculus
9	149	12.4	250	4 Q8NPH7	Q8nph7 homo sapien
10	127	10.5	330	4 Q8IZK7	Q8izk7 homo sapien
11	91	7.6	793	4 Q13876	Q13876 homo sapien
12	89	7.4	420	16 Q8JQJ6	Q8jqj6 streptomyce
13	88	7.3	402	4 Q8NVB6	Q8nvb6 homo sapien
14	88	7.3	402	4 Q9H7U5	Q9h7u5 homo sapien
15	88	7.3	542	4 Q8N543	Q8n543 homo sapien
16	88	7.3	542	4 Q9H9J9	Q9h9j9 homo sapien

17	88	7.3	542	4 Q9HA87	Q9ha87 homo sapien
18	88	7.3	550	4 Q9HCG0	Q9hcg0 homo sapien
19	85.5	7.1	442	2 Q9F6X7	Q9f6x7 chloroflexu
20	85.5	7.1	1066	16 Q8G5I3	Q8g5i3 bifidobacte
21	85	7.1	767	13 Q9I2I5	Q9i2i5 oncorhynchu
22	84.5	7.0	239	9 Q8SDX2	Q8sdx2 bacteriophu
23	84.5	7.0	380	16 P95190	P95190 mycobacteri
24	84.5	7.0	986	4 Q9UPW8	Q9upw8 homo sapien
25	83.5	6.9	441	2 Q07386	Q07386 lactococcus
26	83	6.9	574	2 Q8VQX9	Q8vqx9 myxococcus
27	83	6.9	1075	3 Q8NJ74	Q8nj74 ustilago ma
28	82.5	6.9	240	10 Q8LFZ7	Q8lfz7 arabidopsis
29	82.5	6.9	404	4 Q8NAL3	Q8nal3 homo sapien
30	82.5	6.9	1119	5 Q9U2G5	Q9u2g5 caenorhabdi
31	82	6.8	513	11 Q8VIH0	Q8vih0 mus musculu
32	81.5	6.8	967	5 Q8I540	Q8i540 plasmodium
33	81	6.7	397	11 Q8K0U6	Q8k0u6 mus musculu
34	81	6.7	891	5 Q0I525	Q0i525 caenorhabdi
35	81	6.7	1333	11 Q8CHB8	Q8chb8 mus musculu
36	80.5	6.7	253	10 Q40898	Q40898 petunia hyb
37	80.5	6.7	678	11 Q8JZP9	Q8jzp9 mus musculu
38	80.5	6.7	1735	11 Q62768	Q62768 rattus norv
39	80	6.6	567	11 Q8CIA2	Q8cla2 mus musculu
40	80	6.6	944	5 Q8T4E9	Q8t4e9 drosophila
41	80	6.6	1776	5 Q8MQW8	Q8mqw8 drosophila
42	80	6.6	1776	5 Q9BK48	Q9bk48 drosophila
43	80	6.6	1776	5 Q9W2T7	Q9w2t7 drosophila
44	80	6.6	1790	5 Q9BK49	Q9bk49 drosophila
45	80	6.6	4379	2 Q9RAH4	Q9rah4 nostoc sp.

ALIGNMENTS

RESULT 1

Q8BZM8	PRELIMINARY;	PRT;	258 AA.
ID	Q8BZM8;		
AC	Q8BZM8;		
DT	01-MAR-2003 (TREMREL. 23, Created)		
DT	01-MAR-2003 (TREMREL. 23, Last sequence update)		
DT	01-MAR-2003 (TREMREL. 23, Last annotation update)		
DE	Tumor necrosis factor (fragment).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	{1}		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;		
RX	MEDLINE=22354683; PubMed=12466851;		
RA	The FANTOM Consortium,		
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs."		
RL	Nature 420:563-573 (2002).		
DR	EMBL; AK034121; BAC28593.1;		
FT	NON_TER		
SQ	SEQUENCE 258 AA; 28604 MW; E6431FE93E782810 CRC64;		
Query Match	75.5%;	Score 909;	DB 11; Length 258;
Best Local Similarity	75.9%;	Pred. No. 7.1e-83;	
Matches: 192;	Conservative 0;	Mismatches 1;	Indels 60; Gaps 4;
QY	40 LLSSFTAMSLYQLAALQADLNLRLMELQSYRGSAATPAAA-----KLLTPAAPRH 90		
Db	6 LLSSFTAMSLYQLAALQADLNLRLMELQSYRGSAATPAAAPELTAGVKLLTPAAPRH 65		
QY	91 NSSRGRNRRAPPGPEETEQQVDLSAPPA-----LRNIIDCQLQIAD 133		
Db	66 NSSRGRNRRAPPGPEETEQQVDLSAPPA-----LRNIIDCQLQIAD 125		
QY	134 SDTPTIRKGYTFVFWLLSFKRGNAL-----YSQVLYTDPFAMGHVI 176		

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Db      DB        109 MPETLPNNSCYSAGIAKLEEGDELQLTIPRENAQISLDGVDVTFFGALKLL 158
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RESULT 7
QBHXJ4 PRELIMINARY; PRT; 288 AA.
ID QBXJ4 AC Q8HJ4
DT DT 01-OCT-2002 (TREMBLrel. 22, Created)
TT 01-WAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
TNF family B cell activation factor.
GN BAFF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RA Schneider K., Kolthow S., Schneider P., Goebel T., Kaspers B.,
   Staeheli P.;
RT "A chicken homolog of the B cell activating factor of the TNF family
   (BAFF)".
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RM EMBL; AF506010; AACW90951.2; -.
SQ SEQUENCE 288 AA; 31629 MW; 8E2F29D249SBB79 CRC64;

Query Match           35.8%; Score 430.5; DB 13; Length 288;
Best Local Similarity 43.4%; Pred.No. 8.1e-35;
Matches 108; Conservative 21; Mismatches 65; Indels 55; Gaps 6

QY    38 AVLSSTFTAMSLIYQAALQLADLMNLRMELQSRYGSA-----TPAAAKLLTPAAPR 88
DB     |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
         |::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
         41 AMLLSSCLAASVLHYTHAITLKTEALARSEL-IYVRARSPLAQPPVPSPGDKKACASVSFF 99

QY    89 PNNSRGHNRRRAPPOPETEQ-DVDL-----SAPPALNIITDCLIQTADSPTP 137
DB     |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
         |::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
         100 LQVSAAGAQRNLPGPSPAESPQEIWRNRNRGRRSIVABETVLQCILTIADSKSD 159

QY    138 TIIRKYTYTVPMLLSFKRGNAL-----YSQVLYTDPIFAMGHVIORKK 180
DB     |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
         |::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
         160 IQOKDDSSIYPMLLSFRGTALLEEQNKIVIKETYGYFYGVGLYTDTTFAMGHLOIRKK 219

QY    181 VHVFGDSLVTLFRCION-----LEEGEIQLAIFPRENAQISRNGDD 223
DB     |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
         |::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
         220 AHVFGGDLTLVTLCRIQNMPQSNPNPCSVTAGIAKLIEGEDLQLTIPRRRAKISLDG 279

QY    224 TFFGALKLL 232
DB     |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
         |::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
         280 TFFGAVALLL 288

RESULT 8
QBXS2 PRELIMINARY; PRT; 410 AA.
ID QBXS2 ID QBXS2
AC AC QBXS2;
DT DT 01-WAR-2003 (TreEMBLrel. 23, Created)
TT 01-WAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-WAR-2003 (TREMBLrel. 23, Last annotation update)
TNF tumor necrosis factor.
GN OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the Riken Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
   60,770 full-length cDNAs.";
```

RL Nature 420:563-573(2002).
DR EMBL: AK044387; BAC31897.1; -- 590A4B74C33PB8D4 CRC64;
SQ SEQUENCE 410 AA; 45881 MW; 590A4B74C33PB8D4 CRC64;

Query Match 12.6%; Score 152; DB 11; Length 410;
Best Local Similarity 27.0%; Pred. No. 1.1e-06;
Matches 62; Conservative 22; Mismatches 70; Indels 76; Gaps 8;

QY 52 QLAALQADLMNRLMELQSYRGVSATPAAKLLTPAAPRHNS-----SRGHR 97
DB 207 QRLCQTEQLSRLREVSRLQSGGSKQ-----GERPQSLWEQSPVLEAKWDGAKSR 261
QY 98 NRRAPPGPEETQDVLDSAPPALRNIIQDCLLIADSDTPTIRKGTFTVPWLLSFKRG 157
DB 262 RRRVLTQKHKHSHVLPV--NITSK-----ADSDV-----TEVMQPVLRGR 306
QY 158 A-----LYSQVLYTDFIFAMGHVQIRKKVHVFGEDELSTLFRCTQ-- 198
DB 307 GLEAQGDIVRVWDTGYLLYSQVLFHDVFTFTMGQVVSRE-----GQGRRETLFRCSR 360
QY 199 -----NLEEGDEIQLAIPRENAQISRNGDDTFFGALKL 231
DB 361 PSDPRAYNSCYSAGVFLHQGDIIITVXIPRANAKLSLSPHGTFLGFKL 410

RESULT 9

QY 98 Q8NPH7 PRELIMINARY; PRT; 250 AA.
AC Q8NPH7;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Proliferation-inducing ligand APRIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyama T., Tsukamoto H., Masumoto K., Himeji D., Hayaashi K.,
RA Harada M., Horiuchi T.;
RL "Genomic structure of APRIL, a proliferation-inducing ligand.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF513501; AAM47279.1; --
DR InterPro; IPR006052; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS0049; TNF 2; 1.
SQ SEQUENCE 250 AA; 27453 MW; AE1E4PDEFD578898 CRC64;

Query Match 12.4%; Score 149; DB 4; Length 250;
Best Local Similarity 25.9%; Pred. No. 1.2e-06;
Matches 58; Conservative 27; Mismatches 73; Indels 66; Gaps 7;

QY 53 LAALQADLMNRLMELQSYRGVSATPAAKLLTPAAPRHNS-----RGHRNRRAPP 103
DB 48 LTOQTEQLSRLREVSRLQSGGSKQ-----GERPQSLWEQSPVLEAKWDGAKSR 107
QY 104 GPEETEQQDVLDSAPPALRNIIQDCLLIADSDTPTIRKGTFTVPWLLSFKRGNA----- 158
DB 108 TQKQKQSHVLPV--INATSK-----DSVD-----TEVMQPALRRGRGLQAG 152
QY 159 -----LYSQVLYTDFIFAMGHVQIRKKVHVFGEDELSTLFRCTQ----- 198
DB 153 YGVRIQDAGVYLLYSQVLFHDVFTFTMGQVVSRE-----GQGRRETLFRCSR 206
QY 199 -----NLEEGDEIQLAIPRENAQISRNGDDTFFGALKL 231
DB 207 AYNSCYSAGVFLHQGDIIITVXIPRANAKLSLSPHGTFLGFKL 250

RESULT 10

QY 29 PITQKEGAVLLSSSFTMSLYQL-----AALQADLMNRLMELQSYRGVSATPAAKLL 82

Q81ZK7
ID Q81ZK7 PRELIMINARY; PRT; 330 AA.
AC Q81ZK7;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE TWE-PRIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22299924; PubMed=12411489;
RA Prader-Balade B., Medena J.P., Lopez-Fraga M., Lozano J.C.,
RA Kofschoten G.M., Picard A., Martinez-A C., Garcia-Sanz J.A.,
RA Hahne M.;
RT "An endogenous hybrid mRNA encodes TWE-PRIL, a functional cell surface
RT TWEAK-APRIL fusion protein.";
RL EMBO J. 21:5711-5720(2002).
DR EMBL: AY081051; AAL90443.1; --
SQ SEQUENCE 330 AA; 36588 MW; FC6F3BCA29C029AE CRC64;

Query Match 10.5%; Score 127; DB 4; Length 330;
Best Local Similarity 27.1%; Pred. No. 0.00027;
Matches 48; Conservative 21; Mismatches 50; Indels 58; Gaps 7;

QY 91 NSSRGHNRRAFPQPEETEQQDVLDSAPPALRNIIQDCLLIADSDTPTIRKGTFTVPWL 150
DB 176 NGERS-RRRAVLTQKQKQSHVLPV--INATSK-----DSVD-----TEVMQ 219
QY 151 LSFKRGNA-----LYSQVLYTDFIFAMGHVQIRKKVHVFGEDELSTL 193
DB 220 PALRRGRGLQAGVGVRIQDAGVYLLYSQVLFHDVFTFTMGQVVSRE-----GQGR 273
QY 194 FRCIQ-----NLEEGDEIQLAIPRENAQISRNGDDTFFGALKL 231
DB 274 FRCIRSMPSHDPAYNSCYSAGVFLHQGDIIITVXIPRANAKLSLSPHGTFLGFKL 330

RESULT 11

Q13876
ID Q13876 PRELIMINARY; PRT; 793 AA.
AC Q13876;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Bone-derived growth factor (Fragment).
GN BPGF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gao C., Zhou H.E., Chen B.-Q., Chung L.W.K.;
RT "Molecular cloning and expression of A novel bone-derived growth
RT factor from a human osteosarcoma cell line.";
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: L42379; AAA89173.1; --
DR HSSP; P00274; 1F6M.
DR Genew; HGNC:9756; OSCN6.
DR InterPro; IPR006662; Thiores.
DR InterPro; IPR006663; Thioresox_dom2.
DR Pfam; PF00085; thiores; 1.
FT NON TER 1
SQ SEQUENCE 793 AA; 86395 MW; 7418928B218A7B62 CRC64;

Query Match 7.6%; Score 91; DB 4; Length 793;

Best Local Similarity 22.7%; Pred. No. 3.5;
Matches 58; Conservative 25; Mismatches 81; Indels 92; Gaps 13;

Db 535 PTPSQ-----ATSWTSLSQLGOLPEGCACAAAPELAMGALELESNRSTLDPKPEMM 587
QY 83 -TPAAPRPHNSRG-----HRNRRAFPGPPE-----ETEQVDLS----- 115
Db 588 KSPNTTTHVPAEGPEASPPKHLPLGLRAAPQEPPEHMAVQVORNEQDEPLQWHLRSET 647
QY 116 -----APPALRNIIQDCILQIADSDTPTIRKGTTFVP--WLLGPK-----RGNALY 160
Db 648 QGLHCWLSPLGRLTASGALW-----RSGAWAAAPSSNSTSLRPAGGFSWTGRGQW 697
QY 161 SQV-----LYTDPFAMGHVIOKKVHVP--GELSIVTLFRCIQNLBEGD 204
Db 698 LQVLOGGFSYLDISLVCGLYPCPSWACWH-----VHLLPGQDKALNRMLATLOPEPPGE 751
QY 205 EQLAIPRENAOISRN 220
Db 752 E-----AGEGAISRH 762

RESULT 12
Q9RJQ6 PRELIMINARY; PRT; 420 AA.
AC Q9RJQ6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative cytochrome P450 157B1.
GN CYP157B1 OR SC00584 OR SCF55.08C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kleser H.M., Denapaita D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kisser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939106; CAB61278.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 420 AA; 45888 MW; F7FE250A4895A640 CRC64;

Query Match 7.4%; Score 89; DB 16; Length 420;
Best Local Similarity 29.5%; Pred. No. 2.4;
Matches 38; Conservative 16; Mismatches 45; Indels 30; Gaps 7;
QY 62 NLRMELQYRGSAATPAAKLITPAAPRPHNSRGHNRRAFPGPPEEQVDLSAPPALR 121
Db 189 DLRLSLDAEGD-DFVAA--YTRVGERIHQLVRKKRER---PGDVTSGMLTHPAGLTDE 242
QY 122 NIIOCLQIADSDTPTIRKGTTFVPWLLSFKRNALYSQVLYTDPFAMGHVIOQRKV 181
Db 243 ELVQQLISVIAAQOQTAN-----WI-----GNTL--RLLLTDERPAL----- 278
QY 182 HVFGDELSL 190
Db 279 NVSGGRLSV 287

RESULT 13
Q9NVB6 PRELIMINARY; PRT; 402 AA.
AC Q9NVB6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ10826.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsumura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masuho Y., Sasaki N.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001688; BAA91838.1; -.
KW Hypothetical protein.
SQ SEQUENCE 402 AA; 46851 MW; BC09C12945BE8146 CRC64;

Query Match 7.3%; Score 88; DB 4; Length 402;
Best Local Similarity 26.1%; Pred. No. 2.8;
Matches 30; Conservative 17; Mismatches 42; Indels 26; Gaps 4;
QY 18 EKGEDMKVGYDPTPQ-----KEGAVLLSSFTAMSLYQLAALQADLMNLRMELQ 68
Db 190 EKAEESKL-----PEILKECMKLFRLSEALFLLLSNFTGLKHLFLAPSEDEMNDKKEAE 243
QY 69 SYRGSAATPAAKLITPAAPRPHNSRG-----HRNRRAFPGPPEEQVDLSAP 117
Db 244 T-----TDITEGTSHPPEPENNQMAISNNQSQSQSQSQSQSQSQSQSQSQSQSQSQ 293

RESULT 14
Q9H7U5 PRELIMINARY; PRT; 402 AA.
AC Q9H7U5;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ14252.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovarian Carcinoma;
RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

1	1103.5	91.7	309	21	RAY87039	Membrane bound mur
2	1103.5	91.7	309	23	ABG56719	Mouse Neurokinine-A
3	1103.5	91.7	309	23	ABJ00461	Murine B lymphocyt
4	1103.5	91.7	309	23	ABJ004719	Human BlyS binding
5	1103.5	91.7	309	23	ABG33578	Murine B lymphocyt
6	1103.5	91.7	309	23	AAU79147	Mouse Neurokinine-A
7	1103.5	91.7	309	23	AAU10943	Mouse AGP-3. Mus
8	1097.5	91.2	309	21	AAAB08263	Amino acid sequenc
9	999	83.0	290	20	RAY04393	Murine Kay-1 ligand.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

XX Farrow SN, Kaptein A, Kitson JDA, Winder AJ;
 XX WPI; 2000-452393/39.
 DR N-PSDB; AAA51863.
 XX New member of the tumor necrosis factor ligand family, known as the D7
 PT ligand, useful in treating cancer, autoimmune disease or diseases
 PT associated with the activation of NF-kappaB
 XX
 PS Disclosure; Fig 6; 48pp; English.
 XX This is the membrane bound murine tumour necrosis factor (TNF)
 CC ligand, D7, D7 or D7 trimers are useful in immunotherapy or treatment of
 CC cancer. D7 is useful against viral diseases or infections, or as a
 CC vaccine adjuvant. It may also be used as an immunogen to produce
 CC antibodies or for screening methods, e.g. for identifying modulators of
 CC D7-receptor interaction. Modulators are useful for immunotherapy,
 CC particularly, in treating inflammation, autoimmune disease, other
 CC diseases associated with activation of transcription factor NF-kappa-B
 CC (e.g. rheumatoid arthritis, neuronal inflammation, asthma), cancers,
 CC infections (e.g. septic shock), or atherosclerosis. The D7 gene is useful
 CC in gene therapy, and may be employed for producing the protein by
 CC recombinant techniques. D7 antibodies are useful for locating the protein
 CC in a tissue, or for purifying the protein.
 XX
 SQ Sequence 309 AA;
 Query Match 91.7%; Score 1103.5; DB 21; Length 309;
 Best Local Similarity 74.4%; Pred. No. 3.2e-116;
 Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
 QY 1 MDESATLPPPCLCFCSEKGEKMDKGYDPTTPQKEGA-----VLSS 43
 DB 1 MDESATLPPPCLCFCSEKGEKMDKGYDPTTPQKEGAFCRDRGLLAATLLALLSS 60
 QY 44 SFTAMSLVQLAALQADLNLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
 DB 61 SFTAMSLVQLAALQADLNLRLMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSR 120
 QY 95 GHRNRRAPGPPETEQDDVLSAPPA-----LRNIIQDCLQLIADSDTP 137
 DB 121 GHRNRRAPGPPETEQDDVLSAPPAAPCLPGCRHSQHDNDGMNLRNIIQDCLQLIADSDTP 180
 QY 138 TIRKGTYYTFVPHLLSFKRGNAL-----YSQVLYTDFIFANGHVIQKK 180
 DB 181 TIRKGTYYTFVPHLLSFKRGNALEKENKIVVRQTGYFFIYSQVLYTDFIFANGHVIQKK 240
 QY 181 VHVFGDELSTLVTLFRQION-----LEEGDEIQLAIPRENAQISRNGDD 223
 DB 241 VHVFGDELSTLVTLFRQIONWPKTLFNNSCYSAGIARLEBGEIQLAIPRENAQISRNGDD 300
 QY 224 TFFGALKL 232
 DB 301 TFFGALKL 309
 RESULT 2
 ABG96469
 ID ABG96469 standard; Protein; 309 AA.
 XX
 AC ABG96469;
 XX
 DT 11-DEC-2002 (first entry)
 XX
 DE Mouse Neutrokin-alpha-like protein fragment #2.
 XX
 KW Neutrokin-alpha; cytokine; autoimmune disease; cancer;
 KW systemic lupus erythematosus; rheumatoid arthritis; Sjogren's syndrome;
 KW B cell cancer; chronic lymphocytic leukaemia; multiple myeloma;
 KW Hodgkin's lymphoma; non-Hodgkin's lymphoma; immunodeficiency;
 KW hypergammaglobulinaemia; hypogammaglobulinaemia; rheumatic heart disease;
 KW diabetes mellitus; autoimmune thyroiditis; Goodpasture's syndrome;

KW Graves' disease; myasthenia gravis; autoimmune haemolytic anaemia;
 KW infertility; chronic active hepatitis; primary biliary cirrhosis;
 KW inflammatory skin disease; psoriasis; allergy; atherosclerosis;
 KW autoimmune thrombocytopaenia; antibody; chromosome 13q34.

OS Mus musculus.

PN US2002115112-A1.

XX 22-AUG-2002.

PD 15-AUG-2001; 2001US-0929493.

XX 22-FEB-2000; 2000US-0507968.

PR 02-MAR-1999; 99US-122389P.

PR 12-MAR-1999; 99US-124097P.

PR 26-MAR-1999; 99US-126599P.

PR 02-APR-1999; 99US-127598P.

PR 16-APR-1999; 99US-130412P.

PR 23-APR-1999; 99US-130696P.

PR 27-APR-1999; 99US-131278P.

PR 29-APR-1999; 99US-131673P.

PR 28-MAY-1999; 99US-136784P.

PR 06-JUL-1999; 99US-142659P.

PR 03-DEC-1999; 99US-168624P.

PR 16-DEC-1999; 99US-171108P.

PR 23-DEC-1999; 99US-171626P.

PR 14-JAN-2000; 2000US-176015P.

PR 15-AUG-2000; 2000US-225628P.

PR 23-AUG-2000; 2000US-227008P.

PR 22-SEP-2000; 2000US-234338P.

PR 17-OCT-2000; 2000US-240806P.

PR 30-NOV-2000; 2000US-250020P.

PR 07-JUN-2001; 2001US-296122P.

PR 13-JUL-2001; 2001US-304809P.

PR 22-FEB-2000; 2000US-0507968.

PR 02-JUN-2000; 2000US-0586288.

PR 08-JUN-2000; 2000US-0588947.

PR 08-JUN-2000; 2000US-0589285.

PR 08-JUN-2000; 2000US-0589286.

PR 08-JUN-2000; 2000US-0589287.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Yu G, Ebner R, Ni J, Rosen CA, Ullrich S;

WPI; 2002-740098/80.

Novel antibody that binds to neurokinine-alpha protein, useful for
 diagnosing and treating diseases or disorders, such as autoimmune
 diseases, lupus erythematosus, rheumatoid arthritis, cancer, or an
 immunodeficiency -

Disclosure; Page 172; 203pp; English.

The invention relates to an isolated antibody (I) or its portion that
 specifically binds to a 285 residue neurokinine-alpha protein sequence
 or a 250 residue APRIL (proliferation inducing ligand) polypeptide
 sequence (S2). Also included are: (1) an antibody or its portion that
 competitively inhibits the specific binding of (I) by at least 50 or
 90 %; (2) a nucleic acid encoding the antibody (I) (or its single chain);
 (3) a vector comprising the nucleic acid; (4) a host cell comprising
 the nucleic acid or vector; and (5) a hybridoma producing the antibody.
 The antibody is useful for treating disease or disorder such as
 autoimmune diseases, systemic lupus erythematosus, rheumatoid arthritis,
 Sjogren's syndrome, cancer, preferably B cell cancer, chronic lymphocytic
 leukaemia, multiple myeloma, Hodgkin's lymphoma and non-Hodgkin's
 lymphoma, an immunodeficiency, hypo or hypergammaglobulinaemia,
 rheumatic heart disease, diabetes mellitus, autoimmune thyroiditis,
 Goodpasture's syndrome, Graves' disease, myasthenia gravis, primary
 haemolytic anaemia, infertility, chronic active hepatitis, primary
 biliary cirrhosis, other disorders such as inflammatory skin diseases
 including psoriasis, allergic conditions, atherosclerosis, antigen-

CC antibody complex mediated diseases and autoimmune thrombocytopaenia. The
 CC antibody is also useful for diagnosing the disease or disorder, by
 CC assaying expression of Neutrokin-alpha and APRIL expression level, in
 CC cells or body fluid of an individual and comparing the levels with a
 CC standard expression level, where an increase or decrease in the assayed
 CC Neutrokin-alpha and APRIL expression level compared to the standard
 CC expression level is indicative of a disease or disorder. The antibody is
 CC also useful for reducing or stimulating immunoglobulin production and to
 CC inhibit or stimulate proliferation of a cell of haematopoietic origin,
 CC preferably a B cell. The gene for Neutrokin-alpha is located on
 CC chromosome 13q34. The present sequence is a non-human Neutrokin-alpha
 CC protein.

XX Sequence 309 AA;
 Query Match 91.7%; Score 1103.5; DB 23; Length 309;
 Best Local Similarity 74.4%; Pred. No. 3.2e-116;
 Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
 QY 1 MDESATLPPPCLCFCSEKGEKMGVYDPIITPQKEGA-----VLLSS 43
 DB 1 MDESATLPPPCLCFCSEKGEKMGVYDPIITPQKEGAWFGICRDRLLAATLLALLSS 60
 QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSGATPAAA-----KLTPAAPRPHNSR 94
 DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSGATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
 QY 95 GHRNRAPFGPEETEEDVDLSAPPA-----LRNIQDCLLIADSDTP 137
 DB 121 GHRNRAPFGPEETEEDVDLSAPPAFCPLGCRHSQHDNDGMNLRNIQDCLLIADSDTP 180
 QY 138 TIRKGTYYFVFWLLSFKRGNAL-----YSQVLYTDFIFAMGHVIQK 180
 DB 181 TIRKGTYYFVFWLLSFKRGNALEKENKIVVQTGYFFIYSQVLYTDFIFAMGHVIQK 240
 QY 181 VHVFGDELSTLTLFRICQN-----LEEGDEIQALAI PRENAQISRNGDD 223
 DB 241 VHVFGDELSTLTLFRICQNMPKTLNPNNSCYSAGIARLEEGDEIQALAI PRENAQISRNGDD 300
 QY 224 TFFGALKLL 232
 DB 301 TFFGALKLL 309

RESULT 3
 ABJ00717
 ID ABJ00717 standard; Protein; 309 AA.

XX
 AC ABJ00717;
 XX 05-SEP-2002 (first entry)

DE Murine B lymphocyte stimulator protein #1.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritis;
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Mus sp.

XX WO200216411-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US25950.

XX 18-AUG-2000; 2000US-226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide -

XX Disclosure; Page 304-306; 387pp; English.

XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production; B cell proliferation
 CC and graft rejection involving administration of BlyS binding polypeptide.
 CC The BlyS binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein.

XX Sequence 309 AA;

Query Match 91.7%; Score 1103.5; DB 23; Length 309;
 Best Local Similarity 74.4%; Pred. No. 3.2e-116;
 Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;

QY 1 MDESATLPPPCLCFCSEKGEKMGVYDPIITPQKEGA-----VLLSS 43
 DB 1 MDESATLPPPCLCFCSEKGEKMGVYDPIITPQKEGAWFGICRDRLLAATLLALLSS 60
 QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSGATPAAA-----KLTPAAPRPHNSR 94
 DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSGATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
 QY 95 GHRNRAPFGPEETEEDVDLSAPPA-----LRNIQDCLLIADSDTP 137
 DB 121 GHRNRAPFGPEETEEDVDLSAPPAFCPLGCRHSQHDNDGMNLRNIQDCLLIADSDTP 180
 QY 138 TIRKGTYYFVFWLLSFKRGNAL-----YSQVLYTDFIFAMGHVIQK 180
 DB 181 TIRKGTYYFVFWLLSFKRGNALEKENKIVVQTGYFFIYSQVLYTDFIFAMGHVIQK 240
 QY 181 VHVFGDELSTLTLFRICQN-----LEEGDEIQALAI PRENAQISRNGDD 223
 DB 241 VHVFGDELSTLTLFRICQNMPKTLNPNNSCYSAGIARLEEGDEIQALAI PRENAQISRNGDD 300
 QY 224 TFFGALKLL 232
 DB 301 TFFGALKLL 309

RESULT 4
 ABP47219
 ID ABP47219 standard; Protein; 309 AA.

XX ABP47219;

XX 19-AUG-2002 (first entry)

XX Human BlyS binding scFv VH CDR3 SEQ ID 3230.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.
 XX PN WO200202641-A1.
 XX PD 10-JAN-2002.
 XX PF 15-JUN-2001; 2001WO-US19110.
 XX PR 16-JUN-2000; 2000US-212210P.
 XX PR 17-OCT-2000; 2000US-240816P.
 XX PR 16-MAR-2001; 2001US-276248P.
 XX PR 21-MAR-2001; 2001US-277379P.
 XX PR 25-MAY-2001; 2001US-293499P.
 XX XX (HUMA-) HUMAN GENOME SCI INC.
 XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX XX WPI; 2002-114799/15.
 XX DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 XX PT the diagnosis and treatment of cancers and immune disorders -
 XX PT the diagnosis and treatment of cancers and immune disorders -
 XX XX Disclosure; Page 3140-3141; 3148pp; English.
 XX XX This invention describes novel antibodies that immunospecifically bind to
 XX CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 XX CC tumour necrosis factor (TNF) super family and induces B cell
 XX CC proliferation and differentiation. The antibodies of the invention have
 XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 XX CC antirheumatic and antiAIDS activity and can be used in vaccines to
 XX CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 XX CC and so may be used to detect and quantitate the presence of Blys in
 XX CC biological samples and may be used in this way to diagnose disease
 XX CC associated with aberrant expression of Blys. They may also be
 XX CC administered to treat diseases associated with aberrant Blys expression
 XX CC and activity such as cancer, immune, and autoimmune disorders and
 XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 XX CC the antibodies and fragments of the antibodies described in the method
 XX CC of the invention.
 XX XX Sequence 309 AA;
 SQ Query Match 91.7%; Score 1103.5; DB 23; Length 309;
 Best Local Similarity 74.4%; Pred. No. 3.2e-116;
 Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
 QY 1 MDESAKTLPPCLCFCEKGEKDMKGVDPITPQKEGA-----VLLSS 43
 DB 1 MDESAKTLPPCLCFCEKGEKDMKGVDPITPQKEGAFCRDRGLLAATLLALLSS 60
 QY 44 SFTAMSLYQLAALQADLMLNRLMELQSYRGSATPAAA-----KLTPAAPRPHNSSR 94
 DB 61 SFTAMSLYQLAALQADLMLNRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSSR 120
 QY 95 GHRNRRAPFGPEETEQQDVLSDAPPA-----LRNIIQDCLQIADSDTP 137
 DB 121 GHRNRRAPFGPEETEQQDVLSDAPPAFCRDRGLLAATLLALLSS 60
 QY 138 TIRKGTTFVFWLLSKFGKGNAL-----YSQVLYTDFPFAMGHVIOQRK 180
 DB 181 TIRKGTTFVFWLLSKFGKGNAL-----YSQVLYTDFPFAMGHVIOQRK 240
 QY 181 VHVFGDELSLVTLPFCIQN-----LEEGDEIQLAIPRENAQISRNGDD 223
 DB 241 VHVFGDELSLVTLPFCIQNPKTLFNNCYSAGIARLEEGDEIQLAIPRENAQISRNGDD 300
 QY 224 TFFGALKLL 232
 |||||

Db 301 TFFGALKLL 309
 RESULT 5
 ABG33578
 ID ABG33578 standard; Protein; 309 AA.
 XX AC ABG33578;
 XX DT 15-JUL-2002 (first entry)
 XX DE Murine B Lymphocyte Stimulator (Blys) protein #1.
 XX KW B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
 XX KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 XX KW synovial fluid; saliva; mucus; mouse.
 XX OS Mus sp.
 XX PN WO200216412-A2.
 XX PD 28-FEB-2002.
 XX PF 17-AUG-2001; 2001WO-US25891.
 XX PR 18-AUG-2000; 2000US-226489P.
 XX XX (DYAX-) DYAX CORP.
 XX XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
 XX XX WPI; 2002-351647/38.
 XX PT New B-lymphocyte stimulator binding polypeptide useful in detecting or
 XX PT isolating Blys or Blys-like polypeptide comprises a specified amino
 XX PT acid sequence -
 XX PS Disclosure; Page 186-188; 269pp; English.
 XX CC The invention relates to a B Lymphocyte Stimulator (Blys) binding
 XX CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
 XX CC reversibly or irreversibly. The binding peptides are used in detection,
 XX CC isolation and/or purification of Blys in a solution such as water or a
 XX CC buffer solution, as well as any fluid and/or cell obtained from an
 XX CC individual biological fluid, body tissue, body cell, cell line, tissue
 XX CC culture or other source containing Blys or Blys-like polypeptides. The
 XX CC biological fluids include sera, plasma, lymph, blood, blood fraction,
 XX CC urine, synovial fluid, spinal fluid, saliva and mucus. Sequences
 XX CC ABG33578 and ABG33579 represent murine B Lymphocyte Stimulator proteins.
 XX XX Sequence 309 AA;
 SQ Query Match 91.7%; Score 1103.5; DB 23; Length 309;
 Best Local Similarity 74.4%; Pred. No. 3.2e-116;
 Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
 QY 1 MDESAKTLPPCLCFCEKGEKDMKGVDPITPQKEGA-----VLLSS 43
 DB 1 MDESAKTLPPCLCFCEKGEKDMKGVDPITPQKEGAFCRDRGLLAATLLALLSS 60
 QY 44 SFTAMSLYQLAALQADLMLNRLMELQSYRGSATPAAA-----KLTPAAPRPHNSSR 94
 DB 61 SFTAMSLYQLAALQADLMLNRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSSR 120
 QY 95 GHRNRRAPFGPEETEQQDVLSDAPPA-----LRNIIQDCLQIADSDTP 137
 DB 121 GHRNRRAPFGPEETEQQDVLSDAPPAFCRDRGLLAATLLALLSS 60
 QY 138 TIRKGTTFVFWLLSKFGKGNAL-----YSQVLYTDFPFAMGHVIOQRK 180
 DB 181 TIRKGTTFVFWLLSKFGKGNAL-----YSQVLYTDFPFAMGHVIOQRK 240
 QY 181 VHVFGDELSLVTLPFCIQN-----LEEGDEIQLAIPRENAQISRNGDD 223
 |||||

Db 241 VHVFGDELSVTLFRCIQNPMTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDD 300
 QY 224 TFFGALKLL 232
 Db 301 TFFGALKLL 309

RESULT 6
 AAU79147
 ID AAU79147 standard; Protein; 309 AA.
 AC AAU79147;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse Neutrokin-alpha-like protein fragment #1.
 XX
 KW Mouse; Neutrokin-alpha-like; antibody; immunogen; B-cell cancer;
 KW autoimmune disease; Sjogren's syndrome; systemic lupus erythematosus;
 KW rheumatoid arthritis; chronic lymphocytic leukaemia; multiple myeloma;
 KW Hodgkin's lymphoma; non-Hodgkin's lymphoma; hypergammaglobulinemia;
 KW APRIL; a proliferation-inducing ligand.
 XX
 OS Mus musculus.
 XX
 PN WO200218620-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 15-AUG-2001; 2001WO-US25549.
 XX
 PR 15-AUG-2000; 2000US-225628P.
 PR 23-AUG-2000; 2000US-227008P.
 PR 22-SEP-2000; 2000US-234338P.
 PR 17-OCT-2000; 2000US-240806P.
 PR 30-NOV-2000; 2000US-250020P.
 PR 06-MAR-2001; 2001US-276248P.
 PR 25-MAY-2001; 2001US-293499P.
 PR 07-JUN-2001; 2001US-296122P.
 PR 13-JUL-2001; 2001US-304809P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Yu G, Ebner R, Ni J, Rosen CA, Ullrich S;
 XX
 XX WPI; 2002-304259/34.
 DR
 XX
 PT An isolated antibody or portion that specifically binds to a protein
 PT useful in the treatment of diseases such as hypergammaglobulinemia and
 PT cancer -
 XX
 PS Disclosure; Page 476-477; 482pp; English.
 XX
 CC The present invention relates to a new antibody, or portion, that
 CC specifically binds to a protein which has a 285 or 250 amino acid
 CC sequence as fully defined in the specification. The antibody of the
 CC invention is useful in treating a disease or disorder such as cancer,
 CC especially B-cell cancer, autoimmune diseases such as Sjogren's
 CC syndrome, systemic lupus erythematosus, rheumatoid arthritis, chronic
 CC lymphocytic leukaemia, multiple myeloma, Hodgkin's lymphoma,
 CC non-Hodgkin's lymphoma or hypergammaglobulinemia, or in diagnosing a
 CC disease or disorder comprising assaying expression of Neutrokin-alpha
 CC and APRIL (a proliferation-inducing ligand) in cells or body fluids using
 CC antibodies and comparing the Neutrokin-alpha and APRIL expression level
 CC with a standard Neutrokin-alpha and APRIL expression level, whereby an
 CC increase or decrease in the assayed Neutrokin-alpha and APRIL expression
 CC level compared to the standard levels is indicative of a disease or
 CC disorder. The present amino acid sequence represents the mouse
 CC Neutrokin-alpha-like protein fragment #1.
 XX
 SQ Sequence 309 AA;

Query Match 91.7%; Score 1103.5; DB 23; Length 309;
 Best Local Similarity 74.4%; Pred. No. 3.2e-116;
 Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;

QY 1 MDESAKTLPPPCLCFCSEKEDMKVGYDPIITPOKEEGR-----VLSS 43
 Db 1 MDESAKTLPPPCLCFCSEKEDMKVGYDPIITPOKEEGR-----VLSS 60

QY 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA-----KLTPAAPRPHNSSR 94
 Db 61 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPELTAGVKLITPAAPRPHNSSR 120

QY 95 GHRNRRAPFGPEETEQQVDLSAPPA-----LRNIQDCQLIADSDTP 137
 Db 121 GHRNRRAPFGPEETEQQVDLSAPPA-----LRNIQDCQLIADSDTP 180

QY 138 TIRKGTTFVFWLLSFKEGNAL-----YSQVLYTDFIFAMGHVIOKK 180
 Db 181 TIRKGTTFVFWLLSFKEGNAL-----YSQVLYTDFIFAMGHVIOKK 240

QY 181 VHVFGDELSVTLFRCIQNPMTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDD 223
 Db 241 VHVFGDELSVTLFRCIQNPMTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDD 300

QY 224 TFFGALKLL 232
 Db 301 TFFGALKLL 309

RESULT 7
 AAU10943
 ID AAU10943 standard; Protein; 309 AA.
 AC AAU10943;
 DT 12-MAR-2002 (first entry)
 XX
 DE Mouse AGP-3.
 XX
 KW Mouse; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
 KW dermatological; neuroprotective; norepinephrine; immunomodulator; metabolic;
 KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
 KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
 KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
 KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
 KW pancreatitis; amyotrophic lateral sclerosis; AIDS; Alzheimer's disease;
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
 KW multiple sclerosis; Parkinson's disease; transgenic animal.
 XX
 OS Mus musculus.
 XX
 PN WO200185782-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 12-FEB-2001; 2001WO-US04568.
 XX
 PR 11-FEB-2000; 2000US-181800P.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Hsu H;
 XX
 XX WPI; 2002-049441/06.
 DR N-PSDB; AAS18545.
 XX
 PT Composition, useful for identifying modulator of receptor for treating
 PT asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor
 PT ligand family member) receptor and encoding nucleic acids -
 XX
 PS Disclosure; Fig 2; 124pp; English.
 XX

CC The invention relates to a composition (I) comprising AGP-3 receptor
 CC (tumour necrosis factor ligand family member) related protein (II)
 CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
 CC assays to identify cells and tissues that express AGP-3R or proteins
 CC related to AGP-3R-related protein and for identifying compounds
 CC (agonists or antagonists) that interact with AGP-3R proteins. (II) is
 CC also useful for identifying intracellular proteins that interact with
 CC the respective cytoplasmic domains by yeast two-hybrid screening
 CC process. (II) is involved in B cell growth, survival and activation
 CC particularly in lymph node, spleen, and Peyer's patches. AGP-3R
 CC agonists and antagonists identified using (II) are used for modulating
 CC B cell response and are used to treat diseases characterised by
 CC inflammatory processes or deregulated immune response such as
 CC rheumatoid arthritis, graft-versus-host disease, Crohn's disease,
 CC lupus, etc. (II) is also useful in the production of hybridoma cells
 CC which are derived from B cells, which involves treating the hybridoma
 CC cells with (II). (II) is useful in the treatment of inflammatory
 CC conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc.
 CC (II), its agonists or antagonists are useful for treating acute
 CC pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
 CC asthma, atherosclerosis, cachexia/anorexia, diabetes, fever,
 CC glomerulonephritis, inflammatory bowel disease, ischaemic injury
 CC including cerebral ischaemia, multiple myeloma, multiple sclerosis,
 CC osteoporosis, Parkinson's disease, pain, reperfusion injury, septic
 CC shock, etc. The nucleic acids are also useful for developing transgenic
 CC animals expressing (II), which are useful for producing the polypeptides
 CC and for the study of in vivo biological activity. The present
 CC sequence represents the amino acid sequence of mouse AGP-3.
 XX

Sequence 309 AA;

Query Match 91.7%; Score 1103.5; DB 23; Length 309;
 Best Local Similarity 74.4%; Pred. No. 3.2e-116; Indels 77; Gaps 5;
 Matches 230; Conservative 0; Mismatches 2;

QY 1 MDESAKTLPPPCLCFCSEKGDGMKGYDPIPTPQKEEGA-----VLSS 43
 DB 1 MDESAKTLPPPCLCFCSEKGDGMKGYDPIPTPQKEEGAFCICRDLRLAATLLALLSS 60
 QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLITPAAPRPHNSR 94
 DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
 QY 95 GHRNRAFPQPEETQDDVLSAPPA-----LRNIQDCLQLIADSDTP 137
 DB 121 GHRNRAFPQPEETQDDVLSAPPAFCPLGCRHSQDDNGMNLRLIQQCLQLIADSDTP 180
 QY 138 TIRKGTTFVFWLLSFKRGNAL-----YSQVLYTDFIFANGHVIQRKK 180
 DB 181 TIRKGTTFVFWLLSFKRGNALEKENIVVRQTYGYFFIYSQVLYTDFIFANGHVIQRKK 240
 QY 181 VHVFGDELSTVTLFRICQN-----LLEGDEIQLAIQPRENAQISRNGDD 223
 DB 241 VHVFGDELSTVTLFRICQNPMTLPNNKSYLAGIARLEGEDEIQLAIQPRENAQISRNGDD 300
 QY 224 TFFGALKLL 232
 DB 301 TFFGALKLL 309

RESULT 8

AAB08262
 ID AAB08262 standard; Protein; 309 AA.
 XX
 AC AAB08262;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Amino acid sequence of a murine AGP-3 polypeptide.
 XX
 KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
 KW type II transmembrane protein; B cell stimulatory factor;

inflammatory disorder; immune disorder; rheumatoid arthritis;
 lupus and graft versus host disease.

Mus sp.

Key Location/Qualifiers
 Domain 1..47 /note= "intracellular domain"
 Region 48..73 /note= "transmembrane region"
 Domain 74..309 /note= "extracellular domain"
 Misc-difference 106 /note= "unspecified amino acid encoded by AAA"
 Misc-difference 271 /note= "Ser encoded by TTG"
 Misc-difference 282 /note= "Glu encoded by GG"
 Misc-difference 295 /note= "Ser encoded by CAC"
 Misc-difference 296 /note= "Arg encoded by GC"

WO2000047740-A2.

17-AUG-2000.

11-FEB-2000; 2000WO-US03653.

12-FEB-1999; 99US-0119906.

18-NOV-1999; 99US-0166271.

(AMGE-) AMGEN INC.

Boyle WJ, Hsu H;

WPI; 2000-558217/51.

N-PSDB; AAA63942.

Novel polypeptides comprising tumour necrosis factor ligand family proteins, useful for treating inflammatory and immune disorders, e.g. rheumatoid arthritis -

Claim 4; Fig 2; 71pp; English.

The present sequence encodes a murine AGP-3 polypeptide. AGP-3 is a tumour necrosis factor (TNF) ligand family member. AGP-3 is a type II transmembrane protein, and is a potent B cell stimulatory factor. Expression of AGP-3 correlates to increases in the number of B cells and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic acids may be used to treat inflammatory and immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and graft versus host disease. The nucleic acids may be used to regulate the expression of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic acids are also useful for the detection of AGP-3 agonists, antagonists and characterizing interactions with AGP-3 related proteins.
 note: this sequence is not specifically claimed. It is only mentioned in the claims, in that a polypeptide that does not comprise the present sequence is claimed.

Sequence 309 AA;

Query Match 91.2%; Score 1097.5; DB 21; Length 309;
 Best Local Similarity 74.1%; Pred. No. 1.6e-115; Indels 77; Gaps 5;
 Matches 229; Conservative 0; Mismatches 3;

QY 1 MDESAKTLPPPCLCFCSEKGDGMKGYDPIPTPQKEEGA-----VLSS 43
 DB 1 MDESAKTLPPPCLCFCSEKGDGMKGYDPIPTPQKEEGAFCICRDLRLAATLLALLSS 60
 QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLITPAAPRPHNSR 94
 DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120

QY 95 GHRNRAPPGPEETEQQVDLSAPPA-----LRNIQDCLQLIADSDTP 137
 |||||
 Db 121 GHRNRAPPGPEETEQQVDLSAPPA-----LRNIQDCLQLIADSDTP 180
 |||||
 QY 138 TIRKCTYTFVPMLLSFKRGNAL-----YSQVLYTDPFIFANGHVIQRKK 180
 |||||
 Db 181 TIRKCTYTFVPMLLSFKRGNAL-----YSQVLYTDPFIFANGHVIQRKK 240
 |||||
 QY 181 VHVFGDELSTLTLFRICION-----LEEGDEIQLAIPRENAQISRNGDD 223
 |||||
 Db 241 VHVFGDELSTLTLFRICION-----LEEGDEIQLAIPRENAQISRNGDD 300
 |||||
 QY 224 TFFGALKUL 232
 |||||
 Db 301 TFFGALKUL 309
 |||||

RESULT 9
 AAY04393
 ID AAY04393 standard; Protein; 290 AA.

XX AC AAY04393;

DT 24-JUN-1999 (first entry)

DE Murine Kay-ligand.

KW Kay-ligand; tumour necrosis factor family; TNF; immune system;
 KW cytokine; autoimmune disease; tissue graft; cancer; cell death.

XX OS Mus sp.

XX PN WO9912964-A2.

XX PD 18-MAR-1999.

XX PF 11-SEP-1998; 98WO-US19037.

XX PR 12-SEP-1997; 97US-0058786.

XX PA (BIOJ) BIOGEN INC.

XX PI Tschopp J;

XX DR WPI; 1999-243715/20.

XX DR N-PSDB; AAX33331.

XX PT New human or murine Kay-ligands, members of the tumour necrosis
 factor family

PS Claim 12; Page 33; 41pp; English.

XX The present sequence represents murine Kay-ligand, which is a member of
 the tumour necrosis factor (TNF) family of cytokines. Pharmaceutical
 compositions containing the Kay-ligand can be used to suppress or
 stimulate the immune system, especially to prevent or reduce the
 severity of autoimmune diseases or response to a tissue graft or to
 treat cancer. An agent capable of interfering with the Kay-ligand can be
 used to induce cell death. The Kay-ligand can also be used to identify
 its receptors.

SQ Sequence 290 AA;

Query Match 83.0%; Score 999; DB 20; Length 290;

Best Local Similarity 71.9%; Pred. No. 2.1e-104;

Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESAKTLPPPCLCFCSEKGDVMKYDPIPTQKEEGA-----VLSS 43
 |||||

Db 1 MDESAKTLPPPCLCFCSEKGDVMKYDPIPTQKEEGA-----VLSS 60
 |||||

QY 44 SFTMSLYQLAALQADLMNLMELQSYRGSATPAAA-----KLLTPAAPRPHNSR 94
 |||||

Db 61 SFTMSLYQLAALQADLMNLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
 |||||
 QY 95 GHRNRAPPGPEETEQQVDLSAPPA-----LRNIQDCLQLIADSDTP 154
 |||||
 Db 121 GHRNRAPPGPEETEQQVDLSAPPA-----LRNIQDCLQLIADSDTP 178
 |||||
 QY 155 RGNAL-----YSQVLYTDPFIFANGHVIQRKKHVFGEDELSTLTLFRCI 197
 |||||
 Db 179 RGNALEEKENKIVVRQTGYFFIYSQVLYTDPFIFANGHVIQRKKHVFGEDELSTLTLFRCI 238
 |||||
 QY 198 QN-----LEEGDEIQLAIPRENAQISRNGDDTFFGALKUL 232
 |||||
 Db 239 QNPKTLPNNCSYSGIARLEEGDEIQLAIPRENAQISRNGDDTFFGALKUL 290
 |||||

RESULT 10

AAW93587

ID AAW93587 standard; Protein; 290 AA.

XX AC AAW93587;

DT 18-JUN-1999 (first entry)

DE Mouse TNRL1-alpha protein.

KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
 KW developmental abnormality; gestational abnormality; prostate cancer;
 KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; mouse; TNRL1-alpha.

XX OS Mus sp.

XX PN WO9911791-A2.

XX PD 11-MAR-1999.

XX PF 04-SEP-1998; 98WO-US18393.

XX PR 05-SEP-1997; 97US-0924634.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Chaudhary PM;

XX DR WPI; 1999-205191/17.

XX DR N-PSDB; AAX23421.

XX PT New Tumour Necrosis Factor family receptor polypeptides and ligands -
 useful for diagnosis and treatment of prostate cancer and
 developmental or gestational abnormalities

PS Claim 34; Fig 11B; 156pp; English.

XX This invention describes isolated Tumour Necrosis Factor (TNF) family
 receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
 fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 their active fragments. APO4 is useful for diagnosing prostate cancer
 by determining levels of APO4 in an individual. Prostate cancer can also
 be treated using APO4 selective binding agents linked to a therapeutic
 moiety. APO4 polypeptides are also useful for identifying selective
 binding agents, useful in diagnosis/treatment of disease by binding of
 agents to the polypeptide/active fragment which is extracellular, or
 expressed on the cell surface. The binding is preferably performed in
 vivo. APO4 polypeptides/active fragments are also useful for screening
 for agonists and antagonists by binding and observing the change in APO4
 activity. Effective pharmacological agents useful in diagnosis or
 treatment of disease are also identified using APO4 polypeptides/active
 fragments and APO4 signal transducer molecules that specifically interact
 with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 activity. The method is performed in vivo or in vitro. APO polypeptides
 are all useful as immunogens for preparing antibodies. APO4 is also

CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.

XX SQ Sequence 290 AA;

Query Match 83.0%; Score 999; DB 20; Length 290;
Best Local Similarity 71.9%; Pred. No. 2.1e-104;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESATLPPCLCFCEKEDMKVGYDPTTPQKEGA-----VLLSS 43
DB 1 MDESATLPPCLCFCEKEDMKVGYDPTTPQKEGAWFGICRDGRLAATLLALLSS 60

QY 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA-----KLLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSR 120

QY 95 GHRNRRAPFGPEETEEDVDLSAPPALRNIIODCLQIADSDPTTIRKGTTFVFPWLLSFK 154
DB 121 GHRNRRAPFGPEETEEDVDLSAPPA--PCLPGCRHSQDDNGMNLNRNTYTFVFPWLLSFK 178

QY 155 RGNAL-----YSQVLYTDFIFAMGHVIOQRKVVHFGDELSTLTPRCI 197
DB 179 RGNALKEENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIOQRKVVHFGDELSTLTPRCI 238

QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMKPTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290

RESULT 11
AAE07880
ID AAE07880 standard; Protein; 290 AA.

XX AC AAE07880;

DT 01-NOV-2001 (first entry)

DE Mouse BAFF protein.

XX Mouse; tumour necrosis factor; TNF; APBF; APRIL; BAFF; therapy; melanoma;
KW immune system-related disorder; cancer; renal cell; breast; stomach;
KW rectal; colon; throat; bladder; ovarian carcinoma; cellular disorder;
KW gastrointestinal; scleroderma; Kaposi's sarcoma; chronic leukaemia;
KW squamous cell carcinoma; hyperproliferative condition; pannus formation;
KW rheumatoid arthritis; post-surgical scarring; fibrosis; liver; uterine;
KW lung; immunodeficiency; inflammatory disease; lymphadenopathy; vulnary;
KW autoimmune disease; graft versus host disease; dermatological;
KW anti-inflammatory; immunosuppressive; cytostatic.

XX OS Mus sp.

XX WO200158949-A2.

PD 16-AUG-2001.

XX 08-FEB-2001; 2001WO-US04121.

XX 11-FEB-2000; 2000US-0181670.

XX (BIOJ) BIOGEN INC.

PI Rennert PD, Thompson JS, Ambrose C, Cachero TG;

XX WPI; 2001-514644/56.

DR N-PSDB; AAD14418.

XX New heteromeric ligand of tumor necrosis factor (TNF) family, useful
PT for diagnosis, treatment of immune system-related disorders in humans,
PT comprises TNF-family member APRIL subunit linked non-covalently to
PT TNF-family member BAFF subunit

PS Claim 2; Fig 2d; 42pp; English.

XX The present invention relates to an isolated heteromeric ligand of
CC tumour necrosis factor (TNF)-family, referred to as APBF comprising a
CC TNF-family member APRIL subunit linked non-covalently to TNF-family
CC member BAFF subunit. APBF is useful for diagnosis or treatment of
CC various immune system-related disorders in mammals, preferably humans.
CC Such disorders include cancer, including cellular disorders, for e.g.
CC renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer,
CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma,
CC colon cancer, bladder cancer, squamous cell carcinoma and
CC gastrointestinal or stomach cancer, cellular hyperproliferative
CC conditions, such as scleroderma, pannus formation in rheumatoid
CC arthritis, post-surgical scarring and lung, liver and uterine fibrosis
CC and immunodeficiencies, inflammatory diseases, lymphadenopathy,
CC autoimmune diseases and graft versus host disease. APBF is also useful
CC for producing monoclonal or polyclonal antibodies and for identifying
CC novel modulators affecting biological function and receptors interacting
CC with APBF. The present sequence is mouse BAFF protein.

XX SQ Sequence 290 AA;

Query Match 83.0%; Score 999; DB 22; Length 290;
Best Local Similarity 71.9%; Pred. No. 2.1e-104;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESATLPPCLCFCEKEDMKVGYDPTTPQKEGA-----VLLSS 43
DB 1 MDESATLPPCLCFCEKEDMKVGYDPTTPQKEGAWFGICRDGRLAATLLALLSS 60

QY 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA-----KLLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSR 120

QY 95 GHRNRRAPFGPEETEEDVDLSAPPALRNIIODCLQIADSDPTTIRKGTTFVFPWLLSFK 154
DB 121 GHRNRRAPFGPEETEEDVDLSAPPA--PCLPGCRHSQDDNGMNLNRNTYTFVFPWLLSFK 178

QY 155 RGNAL-----YSQVLYTDFIFAMGHVIOQRKVVHFGDELSTLTPRCI 197
DB 179 RGNALKEENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIOQRKVVHFGDELSTLTPRCI 238

QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMKPTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290

RESULT 12
ABG96470
ID ABG96470 standard; Protein; 290 AA.

XX AC ABG96470;

DT 11-DEC-2002 (first entry)

DE Mouse Neutrokin-alpha-like protein fragment #3.

XX Neutrokin-alpha; cytokine; autoimmune disease; cancer;
KW systemic lupus erythematosus; rheumatoid arthritis; Sjogren's syndrome;
KW B cell cancer; chronic lymphocytic leukaemia; multiple myeloma;
KW Hodgkin's lymphoma; non-Hodgkin's lymphoma; immunodeficiency;
KW hypergammaglobulinaemia; hypogammaglobulinaemia; rheumatic heart disease;
KW diabetes mellitus; autoimmune thyroiditis; Goodpasture's syndrome;
KW Graves' disease; myasthenia gravis; autoimmune haemolytic anaemia;
KW infertility; chronic active hepatitis; autoimmune biliary cirrhosis;
KW inflammatory skin disease; psoriasis; allergy; atherosclerosis;
KW autoimmune thrombocytopaenia; antibody; chromosome 13q34.

XX OS Mus musculus.

XX US2002115112-A1.

XX 22-AUG-2002.

XX 15-AUG-2001; 2001US-0929493.
XX
XX
PR 22-FEB-2000; 2000US-0507968.
PR 02-MAR-1999; 99US-122388P.
PR 12-MAR-1999; 99US-124097P.
PR 26-MAR-1999; 99US-126599P.
PR 02-APR-1999; 99US-127598P.
PR 16-APR-1999; 99US-130412P.
PR 23-APR-1999; 99US-130696P.
PR 27-APR-1999; 99US-131278P.
PR 29-APR-1999; 99US-131673P.
PR 28-MAY-1999; 99US-136784P.
PR 06-JUL-1999; 99US-142659P.
PR 03-DEC-1999; 99US-168624P.
PR 16-DEC-1999; 99US-171108P.
PR 23-DEC-1999; 99US-171626P.
PR 14-JAN-2000; 2000US-176015P.
PR 15-AUG-2000; 2000US-225628P.
PR 23-AUG-2000; 2000US-227008P.
PR 22-SEP-2000; 2000US-234338P.
PR 17-OCT-2000; 2000US-240806P.
PR 30-NOV-2000; 2000US-250020P.
PR 07-JUN-2001; 2001US-236122P.
PR 13-JUL-2001; 2001US-304809P.
PR 22-FEB-2000; 2000US-0507968.
PR 02-JUN-2000; 2000US-0586288.
PR 08-JUN-2000; 2000US-0588947.
PR 08-JUN-2000; 2000US-0589285.
PR 08-JUN-2000; 2000US-0589286.
PR 08-JUN-2000; 2000US-0589287.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Yu G, Ebner R, Ni J, Rosen CA, Ullrich S;
XX WPI; 2002-740098/80.
XX
XX Novel antibody that binds to neutrokin-alpha protein, useful for
PT diagnosing and treating diseases or disorders, such as autoimmune
PT diseases, lupus erythematosus, rheumatoid arthritis, cancer, or an
PT immunodeficiency -
XX
XX Disclosure; Page 173; 203pp; English.
XX
XX The invention relates to an isolated antibody (I) or its portion that
CC specifically binds to a 285 residue neutrokin-alpha protein sequence
CC or a 250 residue APRIL (proliferation inducing ligand) polypeptide
CC sequence (S2). Also included are: (1) an antibody or its portion that
CC competitively inhibits the specific binding of (I) by at least 50 or
CC 90 %; (2) a nucleic acid encoding the antibody (I) (or its single chain);
CC (3) a vector comprising the nucleic acid; (4) a host cell comprising
CC the nucleic acid or vector; and (5) a hybridoma producing the antibody.
CC The antibody is useful for treating disease or disorder such as
CC autoimmune diseases, systemic lupus erythematosus, rheumatoid arthritis,
CC Sjogren's syndrome, cancer, preferably B cell cancer, chronic lymphocytic
CC leukaemia, multiple myeloma, Hodgkin's lymphoma and non-Hodgkin's
CC lymphoma, an immunodeficiency, hypo or hypergammaglobulinaemia,
CC rheumatic heart disease, diabetes mellitus, autoimmune thyroiditis,
CC Coopers syndrome, Graves' disease, myasthenia gravis, autoimmune
CC haemolytic anaemia, infertility, chronic active hepatitis, primary
CC biliary cirrhosis, other disorders such as inflammatory skin diseases
CC including psoriasis, allergic conditions, atherosclerosis, antigen-
CC antibody complex mediated diseases and autoimmune thrombocytopenia. The
CC antibody is also useful for diagnosing the disease or disorder, by
CC assaying expression of Neutrokin-alpha and APRIL expression level, in
CC cells or body fluid of an individual and comparing the levels with a
CC standard expression level, where an increase or decrease in the assayed
CC Neutrokin-alpha and APRIL expression level compared to the standard
CC expression level in indicative of a disease or disorder. The antibody is
CC also useful for reducing or stimulating immunoglobulin production and to
CC inhibit or stimulate proliferation of a cell of haematopoietic origin,
CC preferably a B cell. The gene for Neutrokin-alpha is located on

CC chromosome 13q34. The present sequence is a non-human Neutrokin-alpha
CC protein.
XX
XX SQ Sequence 290 AA;
Query Match 83.0%; Score 999; DB 23; Length 290;
Best Local Similarity 71.9%; Pred. No. 2.1e-104;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;
QY 1 MDESAKTLPPPCLCFCSEKGEDMKGYDPIITPQKEGA-----VLLSS 43
DB 1 MDESAKTLPPPCLCFCSEKGEDMKGYDPIITPQKEGAWFGICRGLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMLNRMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMLNRMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRRAPFGPTEQDQVDSAPPALRNIIQDCLQIADSDTPTTKGTYTFVPWLLSPK 154
DB 121 GHRNRRAPFGPTEQDQVDSAPPA--PCLPGCRHSQHDDNGMNLNRNTYTFVPWLLSPK 178
QY 155 RGNAL-----YSQVLYTDPIFAMGHVIOQRKKVHVGDELSTLTLFRCI 197
DB 179 RGNALKEENKIVRQTGYFFIYSQVLYTDPIFAMGHVIOQRKKVHVGDELSTLTLFRCI 238
QY 198 QN-----LEEGBIQLAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMKPTLPNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 290
RESULT 13
ABJ00718
ID ABJ00718 standard; Protein; 290 AA.
XX
XX AC ABJ00718;
XX
XX DT 05-SEP-2002 (first entry)
XX
XX DE Murine B lymphocyte stimulator protein #2.
XX
XX KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antischmatic; anti-allergic; thymostimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX OS Mus sp.
XX
XX PN WO200216411-A2.
XX
XX PD 28-FEB-2002.
XX
XX PF 17-AUG-2001; 2001WO-US25850.
XX
XX PR 18-AUG-2000; 2000US-226700P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Belzer JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
XX
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide -
XX Disclosure; Page 306-307; 387pp; English.
XX
XX CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B

CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hyperagmaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein.

XX Sequence 290 AA;

Query Match 83.0%; Score 999; DB 23; Length 290;
 Best Local Similarity 71.9%; Pred. No. 2.1e-104;
 Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLSS 43
 |||||
 DB 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGAWFGICRGRLLAATLLALLSS 60
 |||||

QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAA-----KLTPAAPRPHNSR 94
 |||||
 DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSR 120
 |||||

QY 95 GHRNRRAPFPGETEQDVLSDAPPALRNIIQDCLQIADSDPTTIRKGYTFVFWLLSPK 154
 |||||
 DB 121 GHRNRRAPFPGETEQDVLSDAPPA--PCLPCRHSQHDNGMNLNRNTYTFVFWLLSPK 178
 |||||

QY 155 RGNAL-----YSQVLYTDPIFAMGHVIRKQKHVFGDELSTLTLFRCI 197
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 DB 179 RGNALKEENKIVVRQGTGYFFIYSQVLYTDPIFAMGHVIRKQKHVFGDELSTLTLFRCI 238
 |||||

QY 198 QN-----LEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 232
 |||||
 DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 290
 |||||

RESULT 14
 ABP47220
 ID ABP47220 standard; Protein; 290 AA.
 AC ABP47220;
 XX
 XX 19-AUG-2002 (first entry)
 XX Human Blys binding scFv VH CDR3 SEQ ID 3231.
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX Homo sapiens.
 XX WO200202641-A1.
 XX 10-JAN-2002.
 XX 15-JUN-2001; 2001WO-US19110.
 XX 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI; 2002-114799/15.
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX Disclosure; Page 3141-3142; 3148pp; English.
 PS This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

XX Sequence 290 AA;

Query Match 83.0%; Score 999; DB 23; Length 290;
 Best Local Similarity 71.9%; Pred. No. 2.1e-104;
 Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLSS 43
 |||||
 DB 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGAWFGICRGRLLAATLLALLSS 60
 |||||

QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAA-----KLTPAAPRPHNSR 94
 |||||
 DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSR 120
 |||||

QY 95 GHRNRRAPFPGETEQDVLSDAPPALRNIIQDCLQIADSDPTTIRKGYTFVFWLLSPK 154
 |||||
 DB 121 GHRNRRAPFPGETEQDVLSDAPPA--PCLPCRHSQHDNGMNLNRNTYTFVFWLLSPK 178
 |||||

QY 155 RGNAL-----YSQVLYTDPIFAMGHVIRKQKHVFGDELSTLTLFRCI 197
 |||||
 DB 179 RGNALKEENKIVVRQGTGYFFIYSQVLYTDPIFAMGHVIRKQKHVFGDELSTLTLFRCI 238
 |||||

QY 198 QN-----LEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 232
 |||||
 DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 290
 |||||

RESULT 15
 ABG33579
 ID ABG33579 standard; Protein; 290 AA.
 XX ABG33579;
 XX 15-JUL-2002 (first entry)
 XX Murine B Lymphocyte Stimulator (Blys) protein #2.
 XX B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus; mouse.
 XX Mus sp.
 OS WO200216412-A2.
 PN 28-FEB-2002.
 XX

XX 17-AUG-2001; 2001WO-US25891.
XX
XX 18-AUG-2000; 2000US-226489P.
XX
XX (DYAX-) DYAX CORP.
XX
XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
XX
XX WPI; 2002-351647/38.
XX
XX New B-lymphocyte stimulator binding polypeptide useful in detecting or
PT isolating Blys or Blys-like polypeptide comprises a specified amino
PT acid sequence
XX
XX
PS Disclosure; Page 188-189; 269pp; English.
XX
XX The invention relates to a B Lymphocyte Stimulator (Blys) binding
CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
CC reversibly or irreversibly. The binding peptides are used in detection,
CC isolation and/or purification of Blys in a solution such as water or a
CC buffer solution, as well as any fluid and/or cell obtained from an
CC individual biological fluid, body tissue, body cell, cell line, tissue
CC culture or other source containing Blys or Blys-like polypeptides. The
CC biological fluids include sera, plasma, lymph, blood, blood fraction,
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
CC ABG33578 and ABG33579 represent murine B Lymphocyte Stimulator proteins.
XX
SQ Sequence 290 AA;
Query Match 83.0%; Score 999; DB 23; Length 290;
Best Local Similarity 71.9%; Pred. No. 2.1e-104;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;
QY 1 MDESAKTLPPPCLCFCSEKGEKMGVGYDPTITPQKEGA-----VLSS 43
DB 1 MDESAKTLPPPCLCFCSEKGEKMGVGYDPTITPQKEGA-----VLSS 60
QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRRAPFPGETEQDVLDSAPPALRNIIQCLQLIADSDPTTIRKGYTFVFPWLLSFK 154
DB 121 GHRNRRAPFPGETEQDVLDSAPPA--PCLPCRHSQHDDNGMNLNRNTYTFVFPWLLSFK 178
QY 155 RGNAL-----YSQVLYTDPPIFAMGHVIOQKKVHVFGEDELSTLTLFRCI 197
DB 179 RGNALEEKENKIVVRQTYGYFFIYSQVLYTDPPIFAMGHVIOQKKVHVFGEDELSTLTLFRCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNPKTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290

Search completed: February 3, 2004, 07:48:17
Job time : 39.6667 secs

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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:45:42 ; Search time 224.782 Seconds
(without alignments)
216.106 Million cell updates/sec

Title: US-09-911-777-2

Perfect score: 1204

Sequence: 1 MDESAKTLPPCLFCSEKSG.....ENAIQSRNGDDTFGALKLL 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1204	100.0	232	9	US-09-911-777-2
2	1204	100.0	232	15	US-10-045-574A-2
3	1103.5	91.7	309	10	US-09-929-493-39
4	1103.5	91.7	309	10	US-09-779-050A-4
5	1103.5	91.7	309	11	US-09-880-748-3230
6	1103.5	91.7	309	11	US-09-932-613-175
7	1103.5	91.7	309	12	US-10-270-487-39
8	1103.5	91.7	309	12	US-09-932-322-175
9	999	83.0	290	10	US-09-929-493-40
10	999	83.0	290	11	US-09-880-748-3231
11	999	83.0	290	11	US-09-932-613-176
12	999	83.0	290	12	US-10-270-487-40
13	999	83.0	290	12	US-09-932-322-176
14	999	83.0	290	15	US-10-214-065-8
15	992.5	82.4	289	10	US-09-929-493-38

16	992.5	82.4	289	12	US-10-270-487-38	Sequence 38, Appl
17	780.5	64.8	239	11	US-09-880-748-3232	Sequence 3232, Ap
18	780.5	64.8	239	11	US-09-932-613-177	Sequence 177, App
19	780.5	64.8	239	12	US-09-932-322-177	Sequence 177, App
20	723.5	60.1	207	11	US-09-880-748-3234	Sequence 3234, Ap
21	723.5	60.1	207	11	US-09-932-613-179	Sequence 179, App
22	723.5	60.1	207	12	US-09-932-322-179	Sequence 179, App
23	696	57.8	218	9	US-09-911-777-1	Sequence 1, Appli
24	681	56.6	220	15	US-10-045-574A-1	Sequence 1, Appli
25	681	56.6	220	11	US-09-880-748-3233	Sequence 3233, Ap
26	681	56.6	220	11	US-09-932-613-178	Sequence 178, App
27	681	56.6	220	12	US-09-932-322-178	Sequence 178, App
28	625	51.9	188	11	US-09-880-748-3235	Sequence 3235, Ap
29	625	51.9	188	11	US-09-932-613-180	Sequence 180, App
30	625	51.9	188	12	US-09-932-322-180	Sequence 180, App
31	622.5	51.7	285	8	US-08-971-317A-2	Sequence 2, Appli
32	622.5	51.7	285	9	US-09-193-663-2	Sequence 2, Appli
33	622.5	51.7	285	9	US-09-877-156-1	Sequence 1, Appli
34	622.5	51.7	285	9	US-09-879-919-23	Sequence 23, Appli
35	622.5	51.7	285	10	US-09-929-493-2	Sequence 2, Appli
36	622.5	51.7	285	10	US-09-779-050A-2	Sequence 2, Appli
37	622.5	51.7	285	11	US-09-302-863-4	Sequence 4, Appli
38	622.5	51.7	285	11	US-09-880-748-3228	Sequence 3228, Ap
39	622.5	51.7	285	11	US-09-932-613-173	Sequence 173, App
40	622.5	51.7	285	12	US-10-137-870-24	Sequence 24, Appl
41	622.5	51.7	285	12	US-10-140-018-24	Sequence 24, Appl
42	622.5	51.7	285	12	US-10-140-021-24	Sequence 24, Appl
43	622.5	51.7	285	12	US-10-140-274-24	Sequence 24, Appl
44	622.5	51.7	285	12	US-10-140-471-24	Sequence 24, Appl
45	622.5	51.7	285	12	US-10-140-807-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-911-777-2
; Sequence 2, Application US/09911777
; Patent No. US20020037852A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: APOTEC S.A.
; APPLICANT: BROWNING, Jeffrey
; APPLICANT: BROWSE, Christine
; APPLICANT: MACKAY, Fabienne
; APPLICANT: TACK, Jurg
; APPLICANT: SCHNEIDER, Pascal
; TITLE OF INVENTION: BUFF, Inhibitors Thereof and Their Use
; FILE REFERENCE: A070 US
; CURRENT APPLICATION NUMBER: US/09/911,777
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 232
; TYPE: PPT
; ORGANISM: Murine

Query Match 100.0%; Score 1204; DB 9; Length 232;

Best Local Similarity 100.0%; Pred. No. 6.4e-120;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDESAKTLPPCLFCSEKSGDMKVGYDPITPQKEGAVLLSSSTAMSLYQLAALQADL 60

Db 1 MDESAKTLPPCLFCSEKSGDMKVGYDPITPQKEGAVLLSSSTAMSLYQLAALQADL 60

QY 61 MNLRLMELQSYRGSATPAAAKLLTPAAPRPHNSRGRHNRRAFPDPEETEODVLSAPPAL 120
DB 61 MNLRLMELQSYRGSATPAAAKLLTPAAPRPHNSRGRHNRRAFPDPEETEODVLSAPPAL 120
QY 121 RNIIOCLQIADSDTPTRKGTTFVFWLLSFKRGALYSQVLYTDFIFAMGHVQRKK 180
DB 121 RNIIOCLQIADSDTPTRKGTTFVFWLLSFKRGALYSQVLYTDFIFAMGHVQRKK 180
QY 181 VHVFGDELSVTLFRCIONLEBDEIQLAIPRENAQISRNGDDTFFGALKLL 232
DB 181 VHVFGDELSVTLFRCIONLEBDEIQLAIPRENAQISRNGDDTFFGALKLL 232

RESULT 2
US-10-045-574A-2
; Sequence 2, Application US/10045574A
; Publication No. US20030095967A1
; GENERAL INFORMATION:
; APPLICANT: MACKAY, Fabienne
; APPLICANT: KALLED, Susan
; TITLE OF INVENTION: BAPF, Inhibitors Thereof and Their Use
; TITLE OF INVENTION: In the Modulation of B-Cell Response and Treatment of
; TITLE OF INVENTION: Autoimmune Disorders
; FILE REFERENCE: 08201.0024-01000
; CURRENT APPLICATION NUMBER: US/10/045,574A
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/911,777
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Murine
US-10-045-574A-2

Query Match 100.0%; Score 1204; DB 15; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.4e-120; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;
QY 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGAVLLSSFTAMSLYQLAALQADL 60
DB 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGAVLLSSFTAMSLYQLAALQADL 60
QY 61 MNLRLMELQSYRGSATPAAAKLLTPAAPRPHNSRGRHNRRAFPDPEETEODVLSAPPAL 120
DB 61 MNLRLMELQSYRGSATPAAAKLLTPAAPRPHNSRGRHNRRAFPDPEETEODVLSAPPAL 120
QY 121 RNIIOCLQIADSDTPTRKGTTFVFWLLSFKRGALYSQVLYTDFIFAMGHVQRKK 180
DB 121 RNIIOCLQIADSDTPTRKGTTFVFWLLSFKRGALYSQVLYTDFIFAMGHVQRKK 180
QY 181 VHVFGDELSVTLFRCIONLEBDEIQLAIPRENAQISRNGDDTFFGALKLL 232
DB 181 VHVFGDELSVTLFRCIONLEBDEIQLAIPRENAQISRNGDDTFFGALKLL 232

RESULT 3
US-09-929-493-39
; Sequence 39, Application US/09929493
; Patent No. US20020115112A1
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant
; FILE REFERENCE: PF343P4
; CURRENT APPLICATION NUMBER: US/09/929,493

; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,628
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/227,008
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/234,338
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/240,806
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/250,020
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/296,122
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/304,809
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-929-493-39

Query Match 91.7%; Score 1103.5; DB 10; Length 309;
Best Local Similarity 74.4%; Pred. No. 4.9e-109; Indels 77; Gaps 5;
Matches 230; Conservative 0; Mismatches 2;
QY 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLLSS 43
DB 1 MDESAKTLPPCLCFCEKGEKMGVYDPTTPQKEGANWFCRDLRLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMLRLMELQSYRGSATPAAA-----KULTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMLRLMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRRAFPDPEETEODVLSAPPA-----LRNIIOCLQIADSDTP 137
DB 121 GHRNRRAFPDPEETEODVLSAPPA-----LRNIIOCLQIADSDTP 180
QY 138 TIRKGTTFVFWLLSFKRGAL-----YSQVLYTDFIFAMGHVQRKK 180
DB 181 TIRKGTTFVFWLLSFKRGALBENKIVVRGTGYFFIYSQVLYTDFIFAMGHVQRKK 240
QY 181 VHVFGDELSVTLFRCION-----LEEGDEIQLAIPRENAQISRNGDD 223
DB 241 VHVFGDELSVTLFRCIONMPTLPNNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDD 300
QY 224 TFFGALKLL 232
DB 301 TFFGALKLL 309

RESULT 4
US-09-779-050A-4
; Sequence 4, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 309

TYPE: PRT
ORGANISM: Mus musculus
US-09-779-050A-4

Query Match 91.7%; Score 1103.5; DB 10; Length 309;
Best Local Similarity 74.4%; Pred. No. 4.9e-109;
Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
QY 1 MDESATLPPPCLCFCSEKGDGMKVGYDPIIPQKEGA-----VLLSS 43
DB 1 MDESATLPPPCLCFCSEKGDGMKVGYDPIIPQKEGAWFGICRDGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMLNRMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMLNRMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRRAPGPEETEEDVDLSAPPA-----LRNIODCLQIADSDTP 137
DB 121 GHRNRRAPGPEETEEDVDLSAPPAPCLPGCRHSQHDNDGNNLRNIIODCLQIADSDTP 180
QY 138 TIRKGTYYTFVFWLLSFKRGNAL-----YSOVLYTDPFIFAMGHVIOQRK 180
DB 181 TIRKGTYYTFVFWLLSFKRGNALEKENKIVVROTGYFFIYSQVLYTDPFIFAMGHVIOQRK 240
QY 181 VHVFGDELSLVTLPFCIQN-----LEEDEIQALAI PRENAQISRNGDD 223
DB 241 VHVFGDELSLVTLPFCIQNMPKTLNNSCYLAGIARLEEGDEIQALAI PRENAQISRNGDD 300
QY 224 TFFGALKLL 232
DB 301 TFFGALKLL 309

RESULT 5

US-09-880-748-3230
Sequence 3230, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3230
LENGTH: 309
TYPE: PRT
ORGANISM: Mus musculus
US-09-880-748-3230

Query Match 91.7%; Score 1103.5; DB 11; Length 309;
Best Local Similarity 74.4%; Pred. No. 4.9e-109;
Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
QY 1 MDESATLPPPCLCFCSEKGDGMKVGYDPIIPQKEGA-----VLLSS 43
DB 1 MDESATLPPPCLCFCSEKGDGMKVGYDPIIPQKEGAWFGICRDGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMLNRMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMLNRMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120

QY 95 GHRNRRAPGPEETEEDVDLSAPPA-----LRNIODCLQIADSDTP 137
DB 121 GHRNRRAPGPEETEEDVDLSAPPAPCLPGCRHSQHDNDGNNLRNIIODCLQIADSDTP 180
QY 138 TIRKGTYYTFVFWLLSFKRGNAL-----YSOVLYTDPFIFAMGHVIOQRK 180
DB 181 TIRKGTYYTFVFWLLSFKRGNALEKENKIVVROTGYFFIYSQVLYTDPFIFAMGHVIOQRK 240
QY 181 VHVFGDELSLVTLPFCIQN-----LEEDEIQALAI PRENAQISRNGDD 223
DB 241 VHVFGDELSLVTLPFCIQNMPKTLNNSCYLAGIARLEEGDEIQALAI PRENAQISRNGDD 300
QY 224 TFFGALKLL 232
DB 301 TFFGALKLL 309

RESULT 6

US-09-932-613-175
Sequence 175, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patent In version 3.1
SEQ ID NO 175
LENGTH: 309
TYPE: PRT
ORGANISM: mouse
US-09-932-613-175

Query Match 91.7%; Score 1103.5; DB 11; Length 309;

Best Local Similarity 74.4%; Pred. No. 4.9e-109;
Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;
QY 1 MDESATLPPPCLCFCSEKGDGMKVGYDPIIPQKEGA-----VLLSS 43
DB 1 MDESATLPPPCLCFCSEKGDGMKVGYDPIIPQKEGAWFGICRDGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMLNRMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLMLNRMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRRAPGPEETEEDVDLSAPPA-----LRNIODCLQIADSDTP 137
DB 121 GHRNRRAPGPEETEEDVDLSAPPAPCLPGCRHSQHDNDGNNLRNIIODCLQIADSDTP 180
QY 138 TIRKGTYYTFVFWLLSFKRGNAL-----YSOVLYTDPFIFAMGHVIOQRK 180
DB 181 TIRKGTYYTFVFWLLSFKRGNALEKENKIVVROTGYFFIYSQVLYTDPFIFAMGHVIOQRK 240
QY 181 VHVFGDELSLVTLPFCIQN-----LEEDEIQALAI PRENAQISRNGDD 223
DB 241 VHVFGDELSLVTLPFCIQNMPKTLNNSCYLAGIARLEEGDEIQALAI PRENAQISRNGDD 300
QY 224 TFFGALKLL 232
DB 301 TFFGALKLL 309

RESULT 7

US-10-270-487-39
Sequence 39, Application US/10270487
Publication No. US20030175208A1
GENERAL INFORMATION:

APPLICANT: Yu et al.
; TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant
; FILE REFERENCE: PF343P5
; CURRENT APPLICATION NUMBER: US/10/270,487
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/368,548
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/336,726
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/331,478
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/330,835
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/329,747
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/329,508
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/929,493
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,628
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/227,008
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/234,338
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 39
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-270-487-39

Query Match 91.7%; Score 1103.5; DB 12; Length 309;
Best Local Similarity 74.4%; Pred. No. 4.9e-109;
Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;

QY 1 MDESAKTLPPPCLCFCSEKGDMDKGYDPTPOKEEGA-----VLSS 43
DB 1 MDESAKTLPPPCLCFCSEKGDMDKGYDPTPOKEEGAFCICRDGRLLAATLLALLSS 60

QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAGAPELTAGVKLTTPAAPRPHNSR 120

QY 95 GHRNRRAPFGPEETEQQDVLSDAPPA-----LRNIQDCLQLIADSDTP 137
DB 121 GHRNRRAPFGPEETEQQDVLSDAPPAPCLPGCRHSQHDNDGMLRNIIQDCLQLIADSDTP 180

QY 138 TIRKGTYYTFVPWLLSFKRGNAL-----YSQVLYTDFIFANGHVIQRKK 180
DB 181 TIRKGTYYTFVPWLLSFKRGNALEKENKIVVROTGYFFIYSQVLYTDFIFANGHVIQRKK 240

QY 181 VHVFGDELVLTLFRCION-----LEEGDEIOLAI PRENAQISRNGDD 223
DB 241 VHVFGDELVLTLFRCIONMPKTLFNNSCYSAGIARLEEGDEIOLAI PRENAQISRNGDD 300

QY 224 TFFGALKLL 232
DB 301 TFFGALKLL 309

RESULT 8
US-09-932-322-175
; Sequence 175, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Ladner, Robert Charles

; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932,322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 175
; LENGTH: 309
; TYPE: PRT
; ORGANISM: mouse
US-09-932-322-175

Query Match 91.7%; Score 1103.5; DB 12; Length 309;
Best Local Similarity 74.4%; Pred. No. 4.9e-109;
Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps 5;

QY 1 MDESAKTLPPPCLCFCSEKGDMDKGYDPTPOKEEGA-----VLSS 43
DB 1 MDESAKTLPPPCLCFCSEKGDMDKGYDPTPOKEEGAFCICRDGRLLAATLLALLSS 60

QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAGAPELTAGVKLTTPAAPRPHNSR 120

QY 95 GHRNRRAPFGPEETEQQDVLSDAPPA-----LRNIQDCLQLIADSDTP 137
DB 121 GHRNRRAPFGPEETEQQDVLSDAPPAPCLPGCRHSQHDNDGMLRNIIQDCLQLIADSDTP 180

QY 138 TIRKGTYYTFVPWLLSFKRGNAL-----YSQVLYTDFIFANGHVIQRKK 180
DB 181 TIRKGTYYTFVPWLLSFKRGNALEKENKIVVROTGYFFIYSQVLYTDFIFANGHVIQRKK 240

QY 181 VHVFGDELVLTLFRCION-----LEEGDEIOLAI PRENAQISRNGDD 223
DB 241 VHVFGDELVLTLFRCIONMPKTLFNNSCYSAGIARLEEGDEIOLAI PRENAQISRNGDD 300

QY 224 TFFGALKLL 232
DB 301 TFFGALKLL 309

RESULT 9
US-09-929-493-40
; Sequence 40, Application US/09929493
; Patent No. US20020115112A1
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant
; FILE REFERENCE: PF343P4
; CURRENT APPLICATION NUMBER: US/09/929,493
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,628
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/227,008
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/234,338
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/240,806
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/250,020
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/296,122
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/304,809
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 290

TYPE: PRT
ORGANISM: Mus Musculus
US-09-929-493-40

Query Match 83.0%; Score 999; DB 10; Length 290;
Best Local Similarity 71.9%; Pred. No. 6.2e-98;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESATLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLLSS 43
DB 1 MDESATLPPCLCFCEKGEKMGVYDPTTPQKEGAWFGICRGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRAPPGPEETEODVLSAPPALRNIIQDCLQIADSDPTTKRGTYTFVPMWLLSFK 154
DB 121 GHRNRAPPGPEETEODVLSAPPA--PCLPGCRHSQHDNGMNLNRNTYTFVPMWLLSFK 178
QY 155 RGNAL-----YSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLVTLPFCI 197
DB 179 RGNALEEKENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLVTLPFCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290

RESULT 10

US-09-880-748-3231
Sequence 3231, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 3231

LENGTH: 290

TYPE: PRT

ORGANISM: Mus musculus

US-09-880-748-3231

Query Match 83.0%; Score 999; DB 11; Length 290;

Best Local Similarity 71.9%; Pred. No. 6.2e-98;

Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESATLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLLSS 43
DB 1 MDESATLPPCLCFCEKGEKMGVYDPTTPQKEGAWFGICRGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRAPPGPEETEODVLSAPPALRNIIQDCLQIADSDPTTKRGTYTFVPMWLLSFK 154
DB 121 GHRNRAPPGPEETEODVLSAPPA--PCLPGCRHSQHDNGMNLNRNTYTFVPMWLLSFK 178

QY 155 RGNAL-----YSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLVTLPFCI 197
DB 179 RGNALEEKENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLVTLPFCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290

RESULT 11

US-09-932-613-176

Sequence 176, Application US/09932613

Publication No. US20030091565A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

APPLICANT: Beltzer, James P.

APPLICANT: Potter, M. Daniel

APPLICANT: Fleming, Tony J.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON

FILE REFERENCE: DYX-025.1 PCT: DYX-025.1 US

CURRENT APPLICATION NUMBER: US/09/932,613

CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458

SOFTWARE: Patent In version 3.1

SEQ ID NO 176

LENGTH: 290

TYPE: PRT

ORGANISM: mouse

US-09-932-613-176

Query Match 83.0%; Score 999; DB 11; Length 290;

Best Local Similarity 71.9%; Pred. No. 6.2e-98;

Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESATLPPCLCFCEKGEKMGVYDPTTPQKEGA-----VLLSS 43
DB 1 MDESATLPPCLCFCEKGEKMGVYDPTTPQKEGAWFGICRGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR 94
DB 61 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRAPPGPEETEODVLSAPPALRNIIQDCLQIADSDPTTKRGTYTFVPMWLLSFK 154
DB 121 GHRNRAPPGPEETEODVLSAPPA--PCLPGCRHSQHDNGMNLNRNTYTFVPMWLLSFK 178
QY 155 RGNAL-----YSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLVTLPFCI 197
DB 179 RGNALEEKENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIOQRKKVHVFGDELSLVTLPFCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290

RESULT 12

US-10-270-487-40

Sequence 40, Application US/10270487

Publication No. US20030175208A1

GENERAL INFORMATION:

APPLICANT: Yu et al.

TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant

FILE REFERENCE: PF343P5

CURRENT APPLICATION NUMBER: US/10/270,487

CURRENT FILING DATE: 2002-10-16

PRIOR APPLICATION NUMBER: 60/368,548

PRIOR FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 60/336,726

PRIOR FILING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: 60/331,478

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/330,835

PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 60/329,747
PRIOR FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/329,508
PRIOR FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/929,493
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,628
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/227,008
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 60/234,338
PRIOR FILING DATE: 2000-09-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 40
LENGTH: 290
TYPE: PRT
ORGANISM: Mus musculus
US-10-270-487-40

Query Match 83.0%; Score 999; DB 12; Length 290;
Best Local Similarity 71.9%; Pred. No. 6.2e-98;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;
QY 1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPTTPQKEGA-----VLLSS 43
DB 1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPTTPQKEGAWFGICRDGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMNLRMELOS YRGSATPAAA-----KLLTPAAPRPHNSSR 94
DB 61 SFTAMSLYQLAALQADLMNLRMELOS YRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSSR 120
QY 95 GHRNRAPFGPEETEQQDVLSDAPPALRNIIQDCLQIADSDPTTIRKGTTFVFPWLLSFK 154
DB 121 GHRNRAPFGPEETEQQDVLSDAPPA--PCLPGCRHSQHDNGMNLNRNTYTFVFPWLLSFK 178
QY 155 RGNAL-----YSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 197
DB 179 RGNAL EKENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290
US-10-270-487-40

RESULT 13
US-09-932-322-176
Sequence 176, Application US/09932322
Publication No. US20030194743A1
GENERAL INFORMATION:
APPLICANT: Dyax Corp.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 176
LENGTH: 290
TYPE: PRT
ORGANISM: mouse
US-09-932-322-176
Query Match 83.0%; Score 999; DB 12; Length 290;
Best Local Similarity 71.9%; Pred. No. 6.2e-98;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;

QY 1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPTTPQKEGA-----VLLSS 43
DB 1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPTTPQKEGAWFGICRDGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMNLRMELOS YRGSATPAAA-----KLLTPAAPRPHNSSR 94
DB 61 SFTAMSLYQLAALQADLMNLRMELOS YRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSSR 120
QY 95 GHRNRAPFGPEETEQQDVLSDAPPALRNIIQDCLQIADSDPTTIRKGTTFVFPWLLSFK 154
DB 121 GHRNRAPFGPEETEQQDVLSDAPPA--PCLPGCRHSQHDNGMNLNRNTYTFVFPWLLSFK 178
QY 155 RGNAL-----YSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 197
DB 179 RGNAL EKENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290
US-10-214-065-8

RESULT 14
US-10-214-065-8
Sequence 8, Application US/10214065
Publication No. US20030023038A1
GENERAL INFORMATION:
APPLICANT: Biogen, Inc.
APPLICANT: Remert, Paul D.
APPLICANT: Thompson, Jeffrey S.
APPLICANT: Ambrose, Christine
APPLICANT: Cachero, Teresa G.
TITLE OF INVENTION: Heterologous Polypeptide of the TNF
FILE REFERENCE: A092 US
CURRENT APPLICATION NUMBER: US/10/214,065
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: 60/181,670
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: PCT/US01/04121
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 290
TYPE: PRT
ORGANISM: Homo sapien
US-10-214-065-8

Query Match 83.0%; Score 999; DB 15; Length 290;
Best Local Similarity 71.9%; Pred. No. 6.2e-98;
Matches 210; Conservative 3; Mismatches 17; Indels 62; Gaps 5;
QY 1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPTTPQKEGA-----VLLSS 43
DB 1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPTTPQKEGAWFGICRDGRLLAATLLALLSS 60
QY 44 SFTAMSLYQLAALQADLMNLRMELOS YRGSATPAAA-----KLLTPAAPRPHNSSR 94
DB 61 SFTAMSLYQLAALQADLMNLRMELOS YRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSSR 120
QY 95 GHRNRAPFGPEETEQQDVLSDAPPALRNIIQDCLQIADSDPTTIRKGTTFVFPWLLSFK 154
DB 121 GHRNRAPFGPEETEQQDVLSDAPPA--PCLPGCRHSQHDNGMNLNRNTYTFVFPWLLSFK 178
QY 155 RGNAL-----YSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 197
DB 179 RGNAL EKENKIVVRQTGYFFIYSQVLYTDFIFAMGHVIQKRVHVFGEDELSTLTLFRCI 238
QY 198 QN-----LEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 232
DB 239 QNMPKTLPNNSCYSAGIARLEEGDEIQIAIPRENAQISRNGDDTFFGALKLL 290
US-10-214-065-8

RESULT 15
US-09-929-493-38
; Sequence 38, Application US/09929493
; Patent No. US20020115112A1
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Neutrokin-alpha and Neutrokin-alpha Splice Variant
; FILE REFERENCE: PF343P4
; CURRENT APPLICATION NUMBER: US/09/929,493
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,628
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/227,008
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/234,338
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/240,806
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/250,020
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/296,122
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/304,809
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-929-493-38

Query Match 82.4%; Score 992.5; DB 10; Length 289;
Best Local Similarity 70.1%; Pred. No. 3.1e-97;
Matches 211; Conservative 3; Mismatches 6; Indels 81; Gaps 6;
QY 1 MDESAKTLPPCLCFCEKEDMKVGYDITPOKEGA-----VLLSS 43
DB 1 MDESAKTLPPCLCFCEKEDMKVGYDITPOKEGAWFGICRDLAATLLALLSS 60
QY 44 SFTAMSLYQALQADLMRLMELQSYRGSAPEAA-----KLTTPAAPRPHNSR 94
DB 61 SFTAMSLYQALQADLMRLMELQSYRGSAPEAAAGAPELTAGVKLLTPAAPRPHNSR 120
QY 95 GHRNRAFFGPEETEODVLSAPPA-----LRNIQDCLQLIADSDTP 137
DB 121 GHRNRAFFGPEETEODVLSAPPAFCPCRHSHQDDNGMNLNIIQDCLQLIADSDTP 180
QY 138 -----TIRKGTTFVFWLLSFKRGNALYSQVLYTDPFAMGHVIOKKVHVFGEDEL 188
DB 181 ALEEKENKIWRQTGYFFI-----YSQVLYTDPFAMGHVIOKKVHVFGEDEL 228
QY 189 SLVTLFRCLQN-----LEEGDEIQIAPRENAQISRNGDDTFFGALKL 231
DB 229 SLVTLFRCLQNPKLPNNSCYSAGIARLEEGDEIQIAPRENAQISRNGDDTFFGALKL 288
QY 232 L 232
DB 289 L 289

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Job time : 225.782 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2004, 07:43:37 ; Search time 14.9511 Seconds
(without alignments)
656.548 Million cell updates/sec

Title: US-09-911-777-2
Perfect score: 1204
Sequence: 1 MDESATLPPCLCFCEKSG.....ENAIQRNGDDTFFGALKL.232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/aaa/5B_COMB.pep:*
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4: /cgn2_6/prodata/1/aaa/6B_COMB.pep:*
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6: /cgn2_6/prodata/1/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	ID	Description
1	992.5	82.4	289	4	US-09-589-287B-38	Sequence 38, Appl
2	992.5	82.4	289	4	US-09-588-947A-38	Sequence 38, Appl
3	622.5	51.7	285	3	US-09-286-529-1	Sequence 1, Appl
4	622.5	51.7	285	4	US-09-589-287B-2	Sequence 2, Appl
5	622.5	51.7	285	4	US-09-496-118B-1	Sequence 1, Appl
6	622.5	51.7	285	4	US-09-565-423-2	Sequence 2, Appl
7	622.5	51.7	285	4	US-09-879-919-23	Sequence 23, Appl
8	622.5	51.7	285	4	US-09-588-947A-2	Sequence 2, Appl
9	582.5	48.4	219	4	US-09-589-287B-30	Sequence 30, Appl
10	582.5	48.4	219	4	US-09-588-947A-30	Sequence 30, Appl
11	578.5	48.0	219	4	US-09-589-287B-28	Sequence 28, Appl
12	578.5	48.0	219	4	US-09-588-947A-28	Sequence 28, Appl
13	531	44.1	266	4	US-09-589-287B-19	Sequence 19, Appl
14	531	44.1	266	4	US-09-879-919-24	Sequence 24, Appl
15	531	44.1	266	4	US-09-588-947A-19	Sequence 19, Appl
16	526	43.7	174	4	US-09-496-118B-5	Sequence 5, Appl
17	464	38.5	155	4	US-09-589-287B-23	Sequence 23, Appl
18	464	38.5	155	4	US-09-588-947A-23	Sequence 23, Appl
19	463	38.5	145	3	US-09-286-529-21	Sequence 21, Appl
20	149	12.4	250	3	US-08-883-086-2	Sequence 2, Appl
21	149	12.4	250	4	US-09-565-423-3	Sequence 3, Appl
22	148	12.3	205	3	US-09-286-529-5	Sequence 5, Appl
23	147	12.2	234	4	US-09-157-864-2	Sequence 2, Appl
24	141	11.7	233	4	US-10-082-260-2	Sequence 2, Appl
25	141	11.7	233	4	US-08-815-783-2	Sequence 2, Appl
26	141	11.7	233	4	US-09-879-919-2	Sequence 2, Appl
27	141	11.7	247	4	US-09-157-864-4	Sequence 4, Appl

28	141	11.7	250	3	US-09-153-927-4	Sequence 4, Appl
29	141	11.7	250	4	US-09-879-919-11	Sequence 11, Appl
30	139	11.5	234	4	US-09-879-919-13	Sequence 13, Appl
31	125	10.4	136	4	US-09-589-287B-20	Sequence 20, Appl
32	125	10.4	136	4	US-09-588-947A-20	Sequence 20, Appl
33	125	10.4	147	3	US-08-883-086-3	Sequence 3, Appl
34	125	10.4	168	4	US-10-082-260-4	Sequence 4, Appl
35	125	10.4	168	4	US-08-815-783-4	Sequence 4, Appl
36	125	10.4	168	4	US-09-879-919-4	Sequence 4, Appl
37	91	7.6	539	2	US-08-735-041A-2	Sequence 2, Appl
38	91	7.6	539	3	US-09-190-476B-2	Sequence 2, Appl
39	91	7.6	539	3	US-09-190-889A-2	Sequence 2, Appl
40	91	7.6	539	3	US-09-190-938B-2	Sequence 2, Appl
41	91	7.6	539	5	PCT-US95-09261-2	Sequence 2, Appl
42	81	6.7	452	4	US-09-252-991A-18948	Sequence 18948, A
43	78.5	6.5	15281	2	US-08-471-119A-2	Sequence 2, Appl
44	77.5	6.4	454	3	US-08-348-518C-4	Sequence 4, Appl
45	77.5	6.4	454	3	US-08-476-509B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-589-287B-38
; Sequence 38, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokine-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 38
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-589-287B-38

Query Match 82.4%; Score 992.5; DB 4; Length 289;
Best Local Similarity 70.1%; Pred. No. 4.1e-107;
Matches 211; Conservative 3; Mismatches 6; Indels 81; Gaps 6;

QY	1	MDESATLPPCLCFCEKSGEDMKVGYDPIFPQKEGA-----VLLSS	43
DB	1	MDESATLPPCLCFCEKSGEDMKVGYDPIFPQKEGAWFGICRDGRLLAATLLALLSS	60
QY	44	STAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLTPAAPRPHNSR	94
DB	61	STAMSLYQLAALQADLNLRLMELQSYRGSATPAAAAGAPELTAGVKLLTPAAPRPHNSR	120
QY	95	GHRNRRAPFGPEETQDQVDLSAPPA-----LRNIIDCLQLIADSDTP	137
DB	121	GHRNRRAPFGPEETQDQVDLSAPPA-----LRNIIDCLQLIADSDTP	180
QY	138	-----TTKRGYTFVPMLLSFGRGNALYSQVLYTDPFAMGHVTRKQKVVFGDEL	188
DB	181	ALEEKENKIVVRQTYGFFI-----YSQVLYTDPFAMGHVTRKQKVVFGDEL	228
QY	189	SLVTLFRCTON-----LEEGDEIQLAIPRENAOISRNGDDTFFGALKL	231
DB	229	SLVTLFRCTONPKTLPNNSCYSAGIARLEEGDEIQLAIPRENAOISRNGDDTFFGALKL	288
QY	232	L 232	
DB	289	L 289	

RESULT 2
US-09-588-947A-38


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; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-589-287B-2

Query Match      51.7%; Score 622.5; DB 4; Length 285;
Best Local Similarity 48.7%; Pred. No. 4.5e-64;
Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;

QY 1 MDESAKTLPPPCLCFCSEKGEDMKV-GYDPTTPQKEGAV-----LLSS 43
DB 1 MDDSTER-EQSRLTSCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSC 59
QY 44 SFTAMSLYQLAALQADLMNLMELQSYRGSATPAAA-----KLLTPAA 86
DB 60 CLTVSVFYQVAALQDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
QY 87 PRPHNSSRGRNRRAPPGPEETEQQVDLSAPPALNIIQDCLLIADSDTPTIRKGT 146
DB 120 PGEGNSSQNSRNRKRAVQGPET-----VTQDCLLIADSETPTIQGSYTF 165
QY 147 VPMLLSEKRGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
DB 166 VPMLLSFKRGSALBEKENKILVKETGYFFYQGVLYTDKTYAMGHVIOKKVHVFGDELS 225
QY 190 LVTFLPRCIQN-----LEEDEIQLAIPRENAQISRNNGDDTFFGALKIL 232
DB 226 LVTFLPRCIQNMPETLPNNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDDVTFFGALKIL 285

RESULT 5
US-09-496-118B-1
; Sequence 1, Application US/09496118B
; Patent No. 6475986
; ORGANISM: human
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat B.
; TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
; FILE OF INVENTION: Apoptosis
; FILE REFERENCE: D6206
; CURRENT APPLICATION NUMBER: US/09/496,118B
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 60/118,531
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 1
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: amino acid sequence of THANK protein
US-09-496-118B-1

Query Match      51.7%; Score 622.5; DB 4; Length 285;
Best Local Similarity 48.7%; Pred. No. 4.5e-64;
Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;

QY 1 MDESAKTLPPPCLCFCSEKGEDMKV-GYDPTTPQKEGAV-----LLSS 43
DB 1 MDDSTER-EQSRLTSCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSC 59
QY 44 SFTAMSLYQLAALQADLMNLMELQSYRGSATPAAA-----KLLTPAA 86
DB 60 CLTVSVFYQVAALQDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
QY 87 PRPHNSSRGRNRRAPPGPEETEQQVDLSAPPALNIIQDCLLIADSDTPTIRKGT 146
DB 120 PGEGNSSQNSRNRKRAVQGPET-----VTQDCLLIADSETPTIQGSYTF 165
QY 147 VPMLLSEKRGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
DB 166 VPMLLSFKRGSALBEKENKILVKETGYFFYQGVLYTDKTYAMGHVIOKKVHVFGDELS 225
QY 190 LVTFLPRCIQN-----LEEDEIQLAIPRENAQISRNNGDDTFFGALKIL 232
DB 226 LVTFLPRCIQNMPETLPNNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDDVTFFGALKIL 285

RESULT 6
US-09-565-423-2
; Sequence 2, Application US/09565423
; Patent No. 6475987
; ORGANISM: human
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-565-423-2

Query Match      51.7%; Score 622.5; DB 4; Length 285;
Best Local Similarity 48.7%; Pred. No. 4.5e-64;
Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;

QY 1 MDESAKTLPPPCLCFCSEKGEDMKV-GYDPTTPQKEGAV-----LLSS 43
DB 1 MDDSTER-EQSRLTSCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSC 59
QY 44 SFTAMSLYQLAALQADLMNLMELQSYRGSATPAAA-----KLLTPAA 86
DB 60 CLTVSVFYQVAALQDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
QY 87 PRPHNSSRGRNRRAPPGPEETEQQVDLSAPPALNIIQDCLLIADSDTPTIRKGT 146
DB 120 PGEGNSSQNSRNRKRAVQGPET-----VTQDCLLIADSETPTIQGSYTF 165
QY 147 VPMLLSEKRGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
DB 166 VPMLLSFKRGSALBEKENKILVKETGYFFYQGVLYTDKTYAMGHVIOKKVHVFGDELS 225
QY 190 LVTFLPRCIQN-----LEEDEIQLAIPRENAQISRNNGDDTFFGALKIL 232
DB 226 LVTFLPRCIQNMPETLPNNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDDVTFFGALKIL 285

RESULT 7
US-09-879-919-23
; Sequence 23, Application US/09879919
; Patent No. 6541224
; ORGANISM: human
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE OF INVENTION: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
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; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-23

Query Match 51.7%; Score 622.5; DB 4; Length 285;
Best Local Similarity 48.7%; Pred. No. 4.5e-64;
Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;
Qy 1 MDESAKTLPPCLCFCEKEDMKV-GYDPTTPOKEGAV-----LLSS 43
Db 1 MDDSTER-EQSLRTSCLKREEMKLCVSLPRKESPSVRSSKDGKLLAATLLALUSC 59
Qy 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLLTPAA 86
Db 60 CLTVVSFYQVAALQDGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
Qy 87 PRPHNSRGHNRRAFPFGPEETEODVLSAPPALNIIQDCQLIADSDTPTIRKGTTF 146
Db 120 PEGNSSQNSRKRVAQGPET-----VTQDCQLIADSETPTIQKSYTF 165
Qy 147 VPWLLSFRKGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
Db 166 VPWLLSFRKGSALBEKENKILVKETGYFFYGVLYTDKTYAMGHLIQRKKVHVFGDELS 225
Qy 190 LVTLFRCIQN-----LEEDEIQLAIPRENAQISRNGDDTFFGALKLL 232
Db 226 LVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDELQALAIPRENAQISLDGDTFFGALKLL 285

RESULT 8
US-09-588-947A-2
; Sequence 2, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659

; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-588-947A-2

Query Match 51.7%; Score 622.5; DB 4; Length 285;
Best Local Similarity 48.7%; Pred. No. 4.5e-64;
Matches 146; Conservative 23; Mismatches 48; Indels 83; Gaps 7;
Qy 1 MDESAKTLPPCLCFCEKEDMKV-GYDPTTPOKEGAV-----LLSS 43
Db 1 MDDSTER-EQSLRTSCLKREEMKLCVSLPRKESPSVRSSKDGKLLAATLLALUSC 59
Qy 44 SFTAMSLYQLAALQADLNLRLMELQSYRGSATPAAA-----KLLTPAA 86
Db 60 CLTVVSFYQVAALQDGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
Qy 87 PRPHNSRGHNRRAFPFGPEETEODVLSAPPALNIIQDCQLIADSDTPTIRKGTTF 146
Db 120 PEGNSSQNSRKRVAQGPET-----VTQDCQLIADSETPTIQKSYTF 165
Qy 147 VPWLLSFRKGNAL-----YSQVLYTDPFAMGHVIOKKVHVFGDELS 189
Db 166 VPWLLSFRKGSALBEKENKILVKETGYFFYGVLYTDKTYAMGHLIQRKKVHVFGDELS 225
Qy 190 LVTLFRCIQN-----LEEDEIQLAIPRENAQISRNGDDTFFGALKLL 232
Db 226 LVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDELQALAIPRENAQISLDGDTFFGALKLL 285

RESULT 9
US-09-589-287B-30
; Sequence 30, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-30

Query Match	48.4%;	Score 582.5;	DB 4;	Length 219;
Best Local Similarity	54.5%;	Pred. No. 1.4e-59;		
Marches 127: Conservative	16:	Mismatches	25:	Indels 65:
Gaps	4:			

Qy	51	YQLAALQADLMNLRMELQSYRGSA	TPAA--	-----KLLTPAAPRPHNSS	93
Dh	1	YVVAVGQDGLASIPAEIOSHFAEKL	PARAPAPKAGICEAPVATGLIKTIF	EPAPAGEGNS	60

QY	94	RGRNRRAFPGEETEQQDVLSAPPALRNIIQDCLQLIADSTPTTKRGTYTFVPWLLSF	153
DB	61	-----VTDNCILQIADSTPTCKGSYTEVPWISF	106

QY
154 KRGNAL-----YSQVLYTDPDIFAMGHVIQRKKHVFGDELSLVTLFRC 196
 ||||| || || ||
107 KCGGII PPPTVVIIIVPPPCGVPIYCQVITXPDVTVMCVHIDPKTKVFGCDLISLVTLFRC 198
 ||||| || || ||

197 IQN-----LEEGDEIQLAIPRENAQISRNGDDTFFGALKLIL 232

RESULT 11

; Sequence 28, Application US/09589287B
 ; Patent No. 6403770
 ; GENERAL INFORMATION:

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; TITLE OF INVENTION: Antibodies to Neutrokinine-alpha
;
; FILE REFERENCE: PP343P3C1
;
; CURRENT APPLICATION NUMBER: US/09/589, 287B

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; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
;
; SOFTWARE: PatentIn ver. 2.1

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;
; LENGTH: 219
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;

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Query Match	48.0%;	Score 578.5;	DB 4;	Length 219;
Best Local Similarity	54.1%;	Pred. No..46-59;		

Qy 51 YQLAALQADLMNLRMELQSYRGSATPAAA : KLLTPAAPRPHNSS 93

QY 94 RGRHNRRAFPGPEETEQQDVL8APPALRN1IQDCLQ1IADSDPTTIRKGTTFVPWLLSF 153

DD	61	QSSRNAGRIQGRDEI	-----VADCLQLADSGHFIIVQNSQALVWDESD	100
QY	154	KRGNAL	-----YSQVLYTDPIFAMGHVIOQRKKVHFGDELSVTLFRC	196

DB	107	RGKSALBEKENLLVREIGIFFLIGQVYDIIDAIITAMGHLIIKRNKNRVFGDELSUVITFAC	168
QY	197	IQN-----LEEGDEITQLAIPRENAQISRNGDDTFFGALKLIL	232

167 IQNMPETLPNNSCYSAGIAKLEEGDELQLAIFKRENAQLSLDGDVTFFGALKLL 219

US-09-588-947A-38

100

;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 08/815,783
;; PRIOR FILING DATE: 1997-03-12
;; PRIOR APPLICATION NUMBER: 60/016,812
;; PRIOR FILING DATE: 1996-03-14
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 24
;; LENGTH: 266
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-879-919-24

Query Match 44.1%; Score 531; DB 4; Length 266;
Best Local Similarity 43.7%; Pred. No. 1.8e-53;
Matches 131; Conservative 20; Mismatches 47; Indels 102; Gaps 7;

QY 1 MDESATLPPCLPCFCEKEDMKV-GYDPTTPQKEGAV-----LLSS 43
DB 1 MDDSTER-EQSRLTSCLEKREMKLKECVSILPRKESPSVRSSKDGKLLAATLLALLSC 59
QY 44 SFTAMSLYQALQADLMNLMELQSYRGSATPAAA-----KLTTPAA 86
DB 60 CLTVSVFYQVAALQGLASRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPA 119
QY 87 PRPHNSSRGRNRRAPFGPEETEODVDLSAPPALRNIIQDCLQIADSDTPTIRKGTYYF 146
DB 120 PEGNSSQNSRNKRAVQGPET-----GSYTF 146
QY 147 VPWLLSFKRGNAL-----YSQVLYTDPIFAMGHVIOQRKKVHVFGEELS 189
DB 147 VPWLLSFKRGSALEKENILVKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGEELS 206
QY 190 LVTLPFCION-----LEEGDEIQLAIPRENAQISRNQDDTFFGALKLL 232
DB 207 LVTLPFCIONMPETLPNNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGSDVTFFGALKLL 266

RESULT 15
US-09-588-947A-19
Sequence 19, Application US/09588947A
Patent No. 6562579
GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
FILE REFERENCE: PF343P3C2
CURRENT APPLICATION NUMBER: US/09/588,947A
PRIOR FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 09/588,947
PRIOR FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 09/507,968
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/122,388
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: 60/124,097
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/126,599
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/127,598
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: 60/130,412
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/130,696
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: 60/131,278
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131,673
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 60/136,784
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/142,659
PRIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: 60/145,824

;; PRIOR FILING DATE: 1999-07-27
;; PRIOR APPLICATION NUMBER: 60/167,239
;; PRIOR FILING DATE: 1999-11-24
;; PRIOR APPLICATION NUMBER: 60/168,624
;; PRIOR FILING DATE: 1999-12-03
;; PRIOR APPLICATION NUMBER: 60/171,108
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: 60/171,626
;; PRIOR FILING DATE: 1999-12-23
;; PRIOR APPLICATION NUMBER: 60/176,015
;; PRIOR FILING DATE: 2000-01-14
;; PRIOR APPLICATION NUMBER: 09/255,794
;; PRIOR FILING DATE: 1999-02-23
;; PRIOR APPLICATION NUMBER: 09/005,874
;; PRIOR FILING DATE: 1998-01-12
;; PRIOR APPLICATION NUMBER: 60/036,100
;; PRIOR FILING DATE: 1997-01-14
;; PRIOR APPLICATION NUMBER: PCT/US96/17957
;; PRIOR FILING DATE: 1996-10-25
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 19
;; LENGTH: 266
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-588-947A-19

Query Match 44.1%; Score 531; DB 4; Length 266;
Best Local Similarity 43.7%; Pred. No. 1.8e-53;
Matches 131; Conservative 20; Mismatches 47; Indels 102; Gaps 7;

QY 1 MDESATLPPCLPCFCEKEDMKV-GYDPTTPQKEGAV-----LLSS 43
DB 1 MDDSTER-EQSRLTSCLEKREMKLKECVSILPRKESPSVRSSKDGKLLAATLLALLSC 59
QY 44 SFTAMSLYQALQADLMNLMELQSYRGSATPAAA-----KLTTPAA 86
DB 60 CLTVSVFYQVAALQGLASRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPA 119
QY 87 PRPHNSSRGRNRRAPFGPEETEODVDLSAPPALRNIIQDCLQIADSDTPTIRKGTYYF 146
DB 120 PEGNSSQNSRNKRAVQGPET-----GSYTF 146
QY 147 VPWLLSFKRGNAL-----YSQVLYTDPIFAMGHVIOQRKKVHVFGEELS 189
DB 147 VPWLLSFKRGSALEKENILVKETGYFFIYQVLYTDKTYAMGHLIQRKKVHVFGEELS 206
QY 190 LVTLPFCION-----LEEGDEIQLAIPRENAQISRNQDDTFFGALKLL 232
DB 207 LVTLPFCIONMPETLPNNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGSDVTFFGALKLL 266

Search completed: February 3, 2004, 07:44:55
Job time : 15.9511 secs

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